

SEQUENCE LISTING

<110> BRAIN BIOTECHNOLOGY RESEARCH AND INFORMATION NETWORK AG  
Verseck, Stefan  
Liebeton, Klaus  
Eck, Jürgen

<120> Nitrile hydratases from metagenome libraries

<130> 009848-0356700

<140> 10/593,357  
<141> 2006-09-18

<150> WO PCT/EP2005/002556  
<151> 2005-03-10

<150> DE 10 2004 013 842.7  
<151> 2004-03-20

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<170> PatentIn version 3.1

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1 5 10 15

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gat cat gac cac gac gtc cac gag gcg atc gag gac cgg gac gag ggt  
Asp His Asp His Asp Val His Glu Ala Ile Glu Asp Arg Asp Glu Gly  
20 25 30

96

ccg ccg tcg gaa ttc gag atc atg agc cgc gcc atg cag gag ctg ctg  
Pro Pro Ser Glu Phe Glu Ile Met Ser Arg Ala Met Gln Glu Leu Leu  
35 40 45

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gaa gag aag ggc gtc gtc acc gcg gag cag gtc cgg cgc agc atg gag	192
Glu Glu Lys Gly Val Val Thr Ala Glu Gln Val Arg Arg Ser Met Glu	
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Lys Phe Glu Glu Glu Leu Pro Tyr Arg Gly Ala Arg Val Val Ala His	
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Cys Ser Cys Tyr Pro Arg Thr Leu Leu Gly Met Pro Pro Thr Trp Tyr	
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145 150 155 160	
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His Asp Ser Asn Ala Asp Met Arg Tyr Val Val Ile Pro Met Arg Pro	
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cag gga acc gag ggc tgg agc gag gag cgg ctc gcg gag ctg ctg acg	624
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35 40 45	

Glu Glu Lys Gly Val Val Thr Ala Glu Gln Val Arg Arg Ser Met Glu  
50 55 60

Lys Phe Glu Glu Glu Leu Pro Tyr Arg Gly Ala Arg Val Val Ala His  
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Ala Trp Thr Asp Pro Glu Phe Lys Lys Arg Leu Leu Ala Asp Gly Lys  
85 90 95

Ala Ala Val Ser Glu Phe Gly Ile Asp Leu Glu Ala Glu Arg Leu Ile  
100 105 110

Ala Val Ala Asn Thr Thr Asp Val His Asn Val Ile Val Cys Thr Leu  
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Cys Ser Cys Tyr Pro Arg Thr Leu Leu Gly Met Pro Pro Thr Trp Tyr  
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Lys Ser Asp Asn Tyr Arg Ser Arg Val Val Tyr Glu Pro Arg Ala Val  
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Leu Lys Glu Phe Gly Thr Val Leu Pro Glu Arg Val Thr Val Arg Val  
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His Asp Ser Asn Ala Asp Met Arg Tyr Val Val Ile Pro Met Arg Pro  
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Gln Gly Thr Glu Gly Trp Ser Glu Glu Arg Leu Ala Glu Leu Leu Thr  
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Ser Ala Met Asn Ile Pro Ala Arg Glu Phe Ala Leu Gln Arg Thr Ala  
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ccg gtc gag cag cgt gtc gac gcg atc cag gcg gcg ctc gac gaa cgc Pro Val Glu Gln Arg Val Asp Ala Ile Gln Ala Ala Leu Asp Glu Arg 35 40 45	144
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gtc gac ccg gaa ttc cgc gcg ctt ctg gcc gac ggt cgc gcc gcc Val Asp Pro Glu Phe Arg Ala Arg Leu Leu Ala Asp Gly Arg Ala Ala 85 90 95	288
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Glu Gln Trp Ile Pro Arg Asn Gly Ala Arg Val Val Ala Lys Ala Trp  
65 70 75 80

Val Asp Pro Glu Phe Arg Ala Arg Leu Leu Ala Asp Gly Arg Ala Ala  
85 90 95

Val Ala Glu Leu Gly Leu Ser Met Pro Lys His His Arg His Leu Val  
100 105 110

Val Leu Glu Asn Thr Pro Ser Val Gln Asn Val Ile Cys Cys Thr Gln  
115 120 125

Cys Ser Cys Thr Ala Phe Thr Ile Ile Gly Leu Pro Pro Asp Trp Tyr  
130 135 140

Lys Asp Leu Glu Tyr Arg Ala Arg Val Val Arg Glu Ser Arg Thr Val  
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Leu Lys Glu Met Gly Leu Asp Leu Pro Arg Asp Val Glu Ile Arg Val  
165 170 175

Trp Asp Thr Thr Ala Asp Thr Arg Tyr Met Val Leu Pro Val Gln Pro  
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Gly Ala Thr Ala Ala Pro Val Gly Leu Ala Lys Ile Ala His Ser His  
20 25 30 96

gag cac cag gcc gtt cct tcc gac ctc acg ctc cgg gtc aag tcc ctc  
Glu His Gln Ala Val Pro Ser Asp Leu Thr Leu Arg Val Lys Ser Leu  
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gaa tcg ctg ctg gtc gag aag ggt ctc gtg gac cgt gag gcc ctc gac Glu Ser Leu Leu Val Glu Lys Gly Leu Val Asp Arg Glu Ala Leu Asp 50 55 60	192
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cgc gtc gtc gcg cg <sup>g</sup> tgg gtc gat ccc gcg tac aaa gag cgc ctg Arg Val Val Ala Arg Ala Trp Val Asp Pro Ala Tyr Lys Glu Arg Leu 85 90 95	288
ctg aaa gac gcc acc tcg gcg atc gcc gag ctc ggt tac acc gga gcc Leu Lys Asp Ala Thr Ser Ala Ile Ala Glu Leu Gly Tyr Thr Gly Ala 100 105 110	336
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ctc gtc gtt tgc acg ctc tgc tcc tgc tat cca tgg ccg gtg ctc ggt Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly 130 135 140	432
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Val Leu Val Asp Thr Tyr Glu Asn Lys Ile Gly Pro Arg Asn Gly Ala  
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Arg Val Val Ala Arg Ala Trp Val Asp Pro Ala Tyr Lys Glu Arg Leu  
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Leu Lys Asp Ala Thr Ser Ala Ile Ala Glu Leu Gly Tyr Thr Gly Ala  
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Gln Gly Glu His Met Val Ala Leu Glu Asn Thr Pro Ala Val His Asn  
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Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly  
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Leu Pro Pro Val Trp Tyr Lys Ser Ala Pro Tyr Arg Ser Arg Ser Val  
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Ile Asp Pro Arg Gly Val Leu Gly Glu Phe Gly Leu Glu Leu Pro Glu  
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Gly Val Glu Val Arg Val Trp Asp Ser Thr Ala Glu Leu Arg Tyr Leu  
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Val Leu Pro Glu Arg Pro Glu Gly Thr Ala Gln Leu Ser Glu Glu Ala  
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Met Pro Asp Asp His Ala His Pro Asp Asp His Ala His Gly Ser Glu  
1 5 10 15

ttg tcc gag atg gat atc cgg gtg cgg gcg ctg gag acc atc ctg acc  
Leu Ser Glu Met Asp Ile Arg Val Arg Ala Leu Glu Thr Ile Leu Thr  
20 25 30

48

96

gag aag ggc tat gtc gat ccg gcg gcg ctc gac cgg atc gtc gag gcg Glu Lys Gly Tyr Val Asp Pro Ala Ala Leu Asp Arg Ile Val Glu Ala 35 40 45	144
ttc gag acc agg atc ggc ccg cat atc ggc gcc cgt atc gtg gca cgg Phe Glu Thr Arg Ile Gly Pro His Ile Gly Ala Arg Ile Val Ala Arg 50 55 60	192
gct tgg gcc gac gcc gaa ttc aag cgg cgg ctg ctc gcc gac gcg acc Ala Trp Ala Asp Ala Glu Phe Lys Arg Arg Leu Leu Ala Asp Ala Thr 65 70 75 80	240
gag gcg gcg aat tcg ctg ggt cat gcg agc ccg gtc ggc agc cat ctg Glu Ala Ala Asn Ser Leu Gly His Ala Ser Pro Val Gly Ser His Leu 85 90 95	288
atc gcg gtc gag aac acg ccg cag acc cac aac ctc gtc gtc tgc act Ile Ala Val Glu Asn Thr Pro Gln Thr His Asn Leu Val Val Cys Thr 100 105 110	336
ttg tgc tcg tgt tat ccg tgg gag gtg ctg gga ttg ccg ccg gtc tgg Leu Cys Ser Cys Tyr Pro Trp Glu Val Leu Gly Leu Pro Pro Val Trp 115 120 125	384
tac aaa tcc gct gcc tac cgc tcg cgc gtg gtg atc gac ccc aag ggc Tyr Lys Ser Ala Ala Tyr Arg Ser Arg Val Val Ile Asp Pro Lys Gly 130 135 140	432
gtc ctc gcc gag ttc ggc ctg acc ctg cca ccg gag acc ggg atc cgc Val Leu Ala Glu Phe Gly Leu Thr Leu Pro Pro Glu Thr Gly Ile Arg 145 150 155 160	480
atc tgg gat tcg acc gcc gag acc cgg ttt ctg gtg gtg ccg atg cgg Ile Trp Asp Ser Thr Ala Glu Thr Arg Phe Leu Val Val Pro Met Arg 165 170 175	528
ccc ccc ggc acc gca ggc tgg agc gag gaa cgg ctc gcc gaa ctc gtc Pro Pro Gly Thr Ala Gly Trp Ser Glu Glu Arg Leu Ala Glu Leu Val 180 185 190	576
acc cgc gac agc atg atc ggc act ggt ctg gcc ggg gcg ccg cag gag Thr Arg Asp Ser Met Ile Gly Thr Gly Leu Ala Gly Ala Pro Gln Glu 195 200 205	624
atg gcc tcg gca tga Met Ala Ser Ala 210	639
<210> 44	
<211> 212	
<212> PRT	
<213> Unknown	
<220>	
<223> Metagenome - alpha unit nitrile hydratase - M2K17	
<400> 44	
Met Pro Asp Asp His Ala His Pro Asp Asp His Ala His Gly Ser Glu 1 5 10 15	
Leu Ser Glu Met Asp Ile Arg Val Arg Ala Leu Glu Thr Ile Leu Thr 20 25 30	
Glu Lys Gly Tyr Val Asp Pro Ala Ala Leu Asp Arg Ile Val Glu Ala 35 40 45	

Phe Glu Thr Arg Ile Gly Pro His Ile Gly Ala Arg Ile Val Ala Arg  
50 55 60

Ala Trp Ala Asp Ala Glu Phe Lys Arg Arg Leu Leu Ala Asp Ala Thr  
65 70 75 80

Glu Ala Ala Asn Ser Leu Gly His Ala Ser Pro Val Gly Ser His Leu  
85 90 95

Ile Ala Val Glu Asn Thr Pro Gln Thr His Asn Leu Val Val Cys Thr  
100 105 110

Leu Cys Ser Cys Tyr Pro Trp Glu Val Leu Gly Leu Pro Pro Val Trp  
115 120 125

Tyr Lys Ser Ala Ala Tyr Arg Ser Arg Val Val Ile Asp Pro Lys Gly  
130 135 140

Val Leu Ala Glu Phe Gly Leu Thr Leu Pro Pro Glu Thr Gly Ile Arg  
145 150 155 160

Ile Trp Asp Ser Thr Ala Glu Thr Arg Phe Leu Val Val Pro Met Arg  
165 170 175

Pro Pro Gly Thr Ala Gly Trp Ser Glu Glu Arg Leu Ala Glu Leu Val  
180 185 190

Thr Arg Asp Ser Met Ile Gly Thr Gly Leu Ala Gly Ala Pro Gln Glu  
195 200 205

Met Ala Ser Ala  
210

<210> 45  
<211> 696  
<212> DNA  
<213> Unknown

<220>  
<223> Metagenome - alpha unit nitrile hydratase - M15aA6

<220>  
<221> CDS  
<222> (1)..(696)

<400> 45

atg cgt tcg ccc ggt gag gcc tca gca acg caa cca gcg ctc att cgg 48  
Met Arg Ser Pro Gly Glu Ala Ser Ala Thr Gln Pro Ala Leu Ile Arg  
1 5 10 15

ctg cat gat cga gct ggc ggc gtt cga tca ttg cgc ggc aaa agg tct 96  
Leu His Asp Arg Ala Gly Gly Val Arg Ser Leu Arg Gly Lys Arg Ser  
20 25 30

cat cgc gcc gga tcg cat cct cgg ggc gct cgc gca tcc gtc gcc aca 144  
His Arg Ala Gly Ser His Pro Arg Gly Ala Arg Ala Ser Val Ala Thr  
35 40 45

ggg tgg ttc gtt ccg ttc tcg gcc agg ctc gcc cg <sup>g</sup> aaa ggc atc gct	192
Gly Trp Phe Val Pro Phe Ser Ala Arg Leu Ala Arg Lys Gly Ile Ala	
50 55 60	
cct ccg gcc gag atc gcc gag cg <sup>g</sup> atc gcc gtc acc gat cgc gca tca	240
Pro Pro Ala Glu Ile Ala Glu Arg Ile Ala Val Thr Asp Arg Ala Ser	
65 70 75 80	
ccg gca atg ggc gct cgc atg gtc gcc aag gcc tgg acc gat ccc gcc	288
Pro Ala Met Gly Ala Arg Met Val Ala Lys Ala Trp Thr Asp Pro Ala	
85 90 95	
ttc cgc acc ctg ctc ttg gaa gac gga acc cgc gcg gca tgg ctc	336
Phe Arg Thr Leu Leu Leu Glu Asp Gly Thr Arg Ala Ala Glu Ser Leu	
100 105 110	
ggc atc atg atg cgc ggc gcc ccg cct ctc ggt gtg ctg gag aat acg	384
Gly Ile Met Met Arg Gly Ala Pro Pro Leu Gly Val Leu Glu Asn Thr	
115 120 125	
ccc gag att cat cac ctc gtc gtt tgc acg ctg tgc agt tgt tac ccg	432
Pro Glu Ile His His Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro	
130 135 140	
cgc gcg gtg ctg ggc tat ccg ccg ttc tgg ttc aaa tcc gcc gcc tac	480
Arg Ala Val Leu Gly Tyr Pro Pro Phe Trp Phe Lys Ser Ala Ala Tyr	
145 150 155 160	
cgg gca cgt gcg gtg cgc gac ccg cgc ggt ctg atc gcc gaa tgg ggc	528
Arg Ala Arg Ala Val Arg Asp Pro Arg Gly Leu Ile Ala Glu Trp Gly	
165 170 175	
acc atg ctg ccc gac gat gtc cgc gtg cga gtg gtg gac agt acg gcc	576
Thr Met Leu Pro Asp Asp Val Arg Val Arg Val Val Asp Ser Thr Ala	
180 185 190	
gac tat cgc tgg atg gtt ctg ccg gtg cgg ccg gcc ggc act gcg ggc	624
Asp Tyr Arg Trp Met Val Leu Pro Val Arg Pro Ala Gly Thr Ala Gly	
195 200 205	
tgg gat gag gag cgc ctc gcc gca atc gta cgc gaa ggc gat atg atc	672
Trp Asp Glu Glu Arg Leu Ala Ala Ile Val Arg Glu Gly Asp Met Ile	
210 215 220	
ggg gtg acc atc cct cgt ctt taa	696
Gly Val Thr Ile Pro Arg Leu	
225 230	

<210> 46  
 <211> 231  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Metagenome - alpha unit nitrile hydratase - M15aA6

<400> 46

Met Arg Ser Pro Gly Glu Ala Ser Ala Thr Gln Pro Ala Leu Ile Arg  
 1 5 10 15

Leu His Asp Arg Ala Gly Gly Val Arg Ser Leu Arg Gly Lys Arg Ser  
 20 25 30

His Arg Ala Gly Ser His Pro Arg Gly Ala Arg Ala Ser Val Ala Thr  
 35 40 45

Gly Trp Phe Val Pro Phe Ser Ala Arg Leu Ala Arg Lys Gly Ile Ala  
50 55 60

Pro Pro Ala Glu Ile Ala Glu Arg Ile Ala Val Thr Asp Arg Ala Ser  
65 70 75 80

Pro Ala Met Gly Ala Arg Met Val Ala Lys Ala Trp Thr Asp Pro Ala  
85 90 95

Phe Arg Thr Leu Leu Leu Glu Asp Gly Thr Arg Ala Ala Glu Ser Leu  
100 105 110

Gly Ile Met Met Arg Gly Ala Pro Pro Leu Gly Val Leu Glu Asn Thr  
115 120 125

Pro Glu Ile His His Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro  
130 135 140

Arg Ala Val Leu Gly Tyr Pro Pro Phe Trp Phe Lys Ser Ala Ala Tyr  
145 150 155 160

Arg Ala Arg Ala Val Arg Asp Pro Arg Gly Leu Ile Ala Glu Trp Gly  
165 170 175

Thr Met Leu Pro Asp Asp Val Arg Val Arg Val Val Asp Ser Thr Ala  
180 185 190

Asp Tyr Arg Trp Met Val Leu Pro Val Arg Pro Ala Gly Thr Ala Gly  
195 200 205

Trp Asp Glu Glu Arg Leu Ala Ala Ile Val Arg Glu Gly Asp Met Ile  
210 215 220

Gly Val Thr Ile Pro Arg Leu  
225 230

<210> 47

<211> 576

<212> DNA

<213> Unknown

<220>

<223> Metagenome - alpha unit nitrile hydratase - M23dA12

<220>

<221> CDS

<222> (1)..(576)

<400> 47

atg cag ttg cgc gtg cgg gcg ctg gaa acc gtt cta gcc gaa aag ggt  
Met Gln Leu Arg Val Arg Ala Leu Glu Thr Val Leu Ala Glu Lys Gly  
1 5 10 15

48

tat ctc gat ccc gcc gcg ctt gat gcg atg atc gaa gcc tac gag acg  
Tyr Leu Asp Pro Ala Ala Leu Asp Ala Met Ile Glu Ala Tyr Glu Thr  
20 25 30

96

cg <sup>g</sup> att g <sup>gg</sup> g <sup>gg</sup> c <sup>cg</sup> cat a <sup>ac</sup> g <sup>gc</sup> g <sup>cg</sup> c <sup>gc</sup> g <sup>tc</sup> g <sup>cc</sup> a <sup>ag</sup> g <sup>cc</sup> t <sup>gg</sup> t <sup>cc</sup>	144
Arg Ile Gly Pro His Asn Gly Ala Arg Val Val Ala Lys Ala Trp Ser	
35 40 45	
gac g <sup>cc</sup> g <sup>ca</sup> t <sup>tc</sup> a <sup>ag</sup> c <sup>ga</sup> g <sup>cg</sup> c <sup>tg</sup> g <sup>tc</sup> g <sup>ag</sup> g <sup>at</sup> g <sup>cg</sup> a <sup>cc</sup> a <sup>ag</sup> g <sup>cc</sup> g <sup>tg</sup>	192
Asp Ala Ala Phe Lys Arg Ala Leu Val Glu Asp Ala Thr Lys Ala Val	
50 55 60	
cag t <sup>cg</sup> t <sup>tc</sup> g <sup>gc</sup> g <sup>tg</sup> g <sup>tc</sup> a <sup>at</sup> c <sup>gc</sup> g <sup>tc</sup> g <sup>gc</sup> g <sup>at</sup> c <sup>ac</sup> c <sup>tg</sup> a <sup>tc</sup> g <sup>cg</sup> g <sup>tc</sup>	240
Gln Ser Phe Gly Val Val Asn Arg Val Gly Asp His Leu Ile Ala Val	
65 70 75 80	
gag a <sup>ac</sup> a <sup>cg</sup> c <sup>cc</sup> a <sup>cg</sup> c <sup>tg</sup> c <sup>ac</sup> a <sup>ac</sup> a <sup>tc</sup> a <sup>tc</sup> g <sup>tg</sup> t <sup>gc</sup> a <sup>cg</sup> t <sup>tg</sup> t <sup>gc</sup> t <sup>cc</sup>	288
Glu Asn Thr Pro Thr Leu His Asn Ile Ile Val Cys Thr Leu Cys Ser	
85 90 95	
t <sup>gc</sup> t <sup>at</sup> c <sup>cg</sup> t <sup>gg</sup> g <sup>aa</sup> g <sup>tg</sup> c <sup>tc</sup> g <sup>gc</sup> c <sup>tg</sup> c <sup>cg</sup> c <sup>cg</sup> g <sup>tc</sup> t <sup>gg</sup> t <sup>ac</sup> a <sup>aa</sup> t <sup>cg</sup>	336
Cys Tyr Pro Trp Glu Val Leu Gly Leu Pro Pro Val Trp Tyr Lys Ser	
100 105 110	
g <sup>cg</sup> c <sup>cc</sup> t <sup>ac</sup> c <sup>gc</sup> t <sup>cg</sup> c <sup>gc</sup> g <sup>cg</sup> g <sup>tc</sup> a <sup>ac</sup> g <sup>ac</sup> c <sup>cg</sup> c <sup>gc</sup> g <sup>gg</sup> g <sup>ta</sup> c <sup>tc</sup> g <sup>cc</sup>	384
Ala Pro Tyr Arg Ser Arg Ala Val Asn Asp Pro Arg Gly Val Leu Ala	
115 120 125	
g <sup>at</sup> t <sup>tc</sup> g <sup>gc</sup> c <sup>tg</sup> a <sup>ag</sup> c <sup>tg</sup> g <sup>cg</sup> c <sup>cg</sup> g <sup>at</sup> a <sup>tg</sup> c <sup>aa</sup> a <sup>tc</sup> c <sup>gt</sup> g <sup>tc</sup> t <sup>gg</sup> g <sup>at</sup>	432
Asp Phe Gly Leu Lys Leu Ala Pro Asp Met Gln Ile Arg Val Trp Asp	
130 135 140	
t <sup>cg</sup> a <sup>cc</sup> g <sup>cc</sup> g <sup>ag</sup> a <sup>cg</sup> c <sup>gc</sup> t <sup>tc</sup> a <sup>tc</sup> g <sup>tg</sup> t <sup>tg</sup> c <sup>cg</sup> a <sup>tg</sup> c <sup>gc</sup> c <sup>cg</sup> g <sup>cc</sup> g <sup>ga</sup>	480
Ser Thr Ala Glu Thr Arg Phe Ile Val Leu Pro Met Arg Pro Ala Gly	
145 150 155 160	
a <sup>cc</sup> g <sup>ac</sup> g <sup>gc</sup> t <sup>gg</sup> a <sup>gc</sup> g <sup>aa</sup> g <sup>aa</sup> a <sup>ag</sup> c <sup>tc</sup> g <sup>cc</sup> g <sup>cg</sup> c <sup>tg</sup> g <sup>tg</sup> a <sup>ca</sup> c <sup>gc</sup> g <sup>at</sup>	528
Thr Asp Gly Trp Ser Glu Glu Lys Leu Ala Ala Leu Val Thr Arg Asp	
165 170 175	
t <sup>gc</sup> a <sup>tg</sup> a <sup>tc</sup> g <sup>gc</sup> a <sup>cc</sup> g <sup>gc</sup> t <sup>ta</sup> c <sup>cc</sup> a <sup>ag</sup> c <sup>aa</sup> c <sup>cc</sup> a <sup>ac</sup> g <sup>ag</sup> g <sup>tc</sup> a <sup>cg</sup> t <sup>aa</sup>	576
Cys Met Ile Gly Thr Gly Leu Pro Lys Gln Pro Asn Glu Val Thr	
180 185 190	

<210> 48  
 <211> 191  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Metagenome - alpha unit nitrile hydratase - M23dA12

<400> 48

Met Gln Leu Arg Val Arg Ala Leu Glu Thr Val Leu Ala Glu Lys Gly  
 1 5 10 15

Tyr Leu Asp Pro Ala Ala Leu Asp Ala Met Ile Glu Ala Tyr Glu Thr  
 20 25 30

Arg Ile Gly Pro His Asn Gly Ala Arg Val Val Ala Lys Ala Trp Ser  
 35 40 45

Asp Ala Ala Phe Lys Arg Ala Leu Val Glu Asp Ala Thr Lys Ala Val  
 50 55 60

Gln Ser Phe Gly Val Val Asn Arg Val Gly Asp His Leu Ile Ala Val  
 65 70 75 80

Glu Asn Thr Pro Thr Leu His Asn Ile Ile Val Cys Thr Leu Cys Ser  
85 90 95

Cys Tyr Pro Trp Glu Val Leu Gly Leu Pro Pro Val Trp Tyr Lys Ser  
100 105 110

Ala Pro Tyr Arg Ser Arg Ala Val Asn Asp Pro Arg Gly Val Leu Ala  
115 120 125

Asp Phe Gly Leu Lys Leu Ala Pro Asp Met Gln Ile Arg Val Trp Asp  
130 135 140

Ser Thr Ala Glu Thr Arg Phe Ile Val Leu Pro Met Arg Pro Ala Gly  
145 150 155 160

Thr Asp Gly Trp Ser Glu Glu Lys Leu Ala Ala Leu Val Thr Arg Asp  
165 170 175

Cys Met Ile Gly Thr Gly Leu Pro Lys Gln Pro Asn Glu Val Thr  
180 185 190

<210> 49

<211> 624

<212> DNA

<213> Unknown

<220>

<223> Metagenome - alpha unit nitrile hydratase - M49bD9

<220>

<221> CDS

<222> (1)..(624)

<400> 49

atg agc gag cac gat tcc ggc gaa agc cat cac cat ccg cag cca cta 48  
Met Ser Glu His Asp Ser Gly Glu Ser His His His Pro Gln Pro Leu  
1 5 10 15

tcg cag gcg gca ttg cgc gcg aag gcg atc gaa tcg ctg ctg gtc gaa 96  
Ser Gln Ala Ala Leu Arg Ala Lys Ala Ile Glu Ser Leu Leu Val Glu  
20 25 30

aag ggg ctg atc gcg acc gac gtg atc gat cgc gtg gta gca acg tac 144  
Lys Gly Leu Ile Ala Thr Asp Val Ile Asp Arg Val Val Ala Thr Tyr  
35 40 45

gag aaa gaa gtc ggg ccg ctc aac ggc gct aaa gtc gtc gcg cgg gcc 192  
Glu Lys Glu Val Gly Pro Leu Asn Gly Ala Lys Val Val Ala Arg Ala  
50 55 60

tgg acc gat ccg gag tac cgc cgc aga ctg ctc aag aac ggc acg gcg 240  
Trp Thr Asp Pro Glu Tyr Arg Arg Arg Leu Leu Lys Asn Gly Thr Ala  
65 70 75 80

gcg att gcc gag ctg gga ttc ggc ggc ttg cag ggc gaa cac atg atg 288  
Ala Ile Ala Glu Leu Gly Phe Gly Gly Leu Gln Gly Glu His Met Met  
85 90 95

gtc gtg gaa aac acg ccg tcc gta cat aac gtg atc tgt tgc acg cta 336  
Val Val Glu Asn Thr Pro Ser Val His Asn Val Ile Cys Cys Thr Leu  
100 105 110

tgc tca tgc tat ccg tgg ccg gtc ctg gga ctt ccg ccg agc tgg tac	384
Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly Leu Pro Pro Ser Trp Tyr	
115 120 125	
aag tcg ctg gcg tat cgt tcg cga atc gtg cgc gag ccg cgc gcc gtc	432
Lys Ser Leu Ala Tyr Arg Ser Arg Ile Val Arg Glu Pro Arg Ala Val	
130 135 140	
ctc ggc gaa ttc ggc ctc gaa ttg ccc gaa acg gtg gaa gtc cgc gta	480
Leu Gly Glu Phe Gly Leu Glu Leu Pro Glu Thr Val Glu Val Arg Val	
145 150 155 160	
tgg gat agc agt gct gag atg cgc tat ctc gtg ttg ccg gag cgt cca	528
Trp Asp Ser Ser Ala Glu Met Arg Tyr Leu Val Leu Pro Glu Arg Pro	
165 170 175	
gcg gga acg acg gag ttg agc gaa gcg gaa ttg gct tca ttg atc acg	576
Ala Gly Thr Thr Glu Leu Ser Glu Ala Glu Leu Ala Ser Leu Ile Thr	
180 185 190	
cgc gat gcc ttg atc ggc gtg gcg aaa gtc gcg gcg cca agc cgc tag	624
Arg Asp Ala Leu Ile Gly Val Ala Lys Val Ala Ala Pro Ser Arg	
195 200 205	

<210> 50

<211> 207

<212> PRT

<213> Unknown

<220>

<223> Metagenome - alpha unit nitrile hydratase - M49bD9

<400> 50

Met Ser Glu His Asp Ser Gly Glu Ser His His His Pro Gln Pro Leu	
1 5 10 15	

Ser Gln Ala Ala Leu Arg Ala Lys Ala Ile Glu Ser Leu Leu Val Glu	
20 25 30	

Lys Gly Leu Ile Ala Thr Asp Val Ile Asp Arg Val Val Ala Thr Tyr	
35 40 45	

Glu Lys Glu Val Gly Pro Leu Asn Gly Ala Lys Val Val Ala Arg Ala	
50 55 60	

Trp Thr Asp Pro Glu Tyr Arg Arg Arg Leu Leu Lys Asn Gly Thr Ala	
65 70 75 80	

Ala Ile Ala Glu Leu Gly Phe Gly Gly Leu Gln Gly Glu His Met Met	
85 80 95	

Val Val Glu Asn Thr Pro Ser Val His Asn Val Ile Cys Cys Thr Leu	
100 105 110	

Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly Leu Pro Pro Ser Trp Tyr	
115 120 125	

Lys Ser Leu Ala Tyr Arg Ser Arg Ile Val Arg Glu Pro Arg Ala Val	
130 135 140	

Leu Gly Glu Phe Gly Leu Glu Leu Pro Glu Thr Val Glu Val Arg Val  
145 150 155 160

Trp Asp Ser Ser Ala Glu Met Arg Tyr Leu Val Leu Pro Glu Arg Pro  
165 170 175

Ala Gly Thr Thr Glu Leu Ser Glu Ala Glu Leu Ala Ser Leu Ile Thr  
180 185 190

Arg Asp Ala Leu Ile Gly Val Ala Lys Val Ala Ala Pro Ser Arg  
195 200 205

<210> 51

<211> 600

<212> DNA

<213> Unknown

<220>

<223> Metagenome - alpha unit nitrile hydratase - M6dE2

<220>

<221> CDS

<222> (1)..(600)

<400> 51

atg agc aac cca cgc cgt cga gaa cg<sup>g</sup> tcg gcc cca ccg gat g<sup>c</sup> g<sup>c</sup> cga  
Met Ser Asn Pro Arg Arg Arg Glu Arg Ser Ala Pro Pro Asp Ala Arg  
1 5 10 15

g<sup>c</sup> aag g<sup>c</sup> g<sup>c</sup> ctc g<sup>c</sup> a gaa g<sup>c</sup> g<sup>c</sup> ctt tcg aag c<sup>a</sup> g<sup>a</sup> g<sup>c</sup> ctc g<sup>t</sup> g<sup>t</sup> c<sup>c</sup> g<sup>a</sup>  
Ala Lys Ala Leu Ala Glu Ala Leu Ser Lys Gln Gly Leu Val Pro Glu  
20 25 30

g<sup>g</sup> g ttc ctc gac cag gtc g<sup>g</sup> t tct cac g<sup>c</sup> g<sup>c</sup> g<sup>c</sup> g<sup>c</sup> tgg agc c<sup>c</sup> g  
Gly Phe Leu Asp Gln Val Gly Ser His Ala Ala Glu Ala Trp Ser Pro  
35 40 45

c<sup>g</sup> a aac g<sup>g</sup> c g<sup>c</sup> a c<sup>g</sup> g<sup>c</sup> g<sup>c</sup> g<sup>c</sup> tgg g<sup>t</sup> gat c<sup>c</sup> c<sup>c</sup> g<sup>a</sup> t<sup>a</sup>c  
Arg Asn Gly Ala Arg Val Val Ala Arg Ala Trp Val Asp Pro Glu Tyr  
50 55 60

c<sup>g</sup> g acg c<sup>c</sup> g<sup>c</sup> ttg ctc g<sup>c</sup> gac g<sup>g</sup> c<sup>a</sup> c<sup>c</sup> g<sup>c</sup> t<sup>t</sup> g<sup>c</sup> g<sup>c</sup> c<sup>t</sup> c<sup>c</sup> g<sup>c</sup>  
Arg Thr Arg Leu Leu Ala Asp Gly Thr Ala Ala Cys Ala Ala Leu Gly  
65 70 75 80

t<sup>a</sup>c g<sup>c</sup> g<sup>g</sup> a c<sup>c</sup> g<sup>c</sup> g<sup>g</sup> a g<sup>a</sup> t<sup>a</sup>c atc g<sup>t</sup> g<sup>t</sup> g<sup>t</sup> a<sup>c</sup> t<sup>t</sup> c<sup>c</sup> g<sup>a</sup> g<sup>c</sup> a<sup>c</sup> g<sup>t</sup>  
Tyr Ala Gly Pro Gln Gly Glu Tyr Ile Val Val Leu Glu Asp Thr Leu  
85 90 95

g<sup>c</sup> c g<sup>t</sup> t<sup>t</sup> c<sup>a</sup> a<sup>c</sup> g<sup>t</sup> atc g<sup>t</sup> t<sup>t</sup> ac<sup>g</sup> c<sup>a</sup> t<sup>t</sup> g<sup>c</sup> t<sup>t</sup> g<sup>t</sup> t<sup>t</sup> a<sup>c</sup> t<sup>t</sup> g<sup>c</sup> t<sup>t</sup>  
Ala Val His Asn Val Ile Val Cys Thr Gln Cys Ser Cys Thr Ala Trp  
100 105 110

c<sup>c</sup> g<sup>t</sup> t<sup>t</sup> g<sup>g</sup> c<sup>t</sup> g<sup>c</sup> c<sup>c</sup> g<sup>a</sup> t<sup>t</sup> t<sup>t</sup> g<sup>t</sup> t<sup>t</sup> a<sup>a</sup> g<sup>t</sup> a<sup>g</sup> t<sup>t</sup> c<sup>c</sup> g<sup>a</sup> g<sup>t</sup> t<sup>t</sup> c<sup>c</sup>  
Pro Val Leu Gly Leu Pro Pro Asp Trp Tyr Lys Ser Pro Glu Tyr Arg  
115 120 125

g<sup>c</sup> c<sup>c</sup> g<sup>t</sup> g<sup>t</sup> c<sup>g</sup> g<sup>g</sup> g<sup>a</sup> c<sup>c</sup> g<sup>c</sup> c<sup>g</sup> g<sup>t</sup> c<sup>t</sup> t<sup>c</sup> g<sup>c</sup> g<sup>a</sup> a<sup>t</sup> g<sup>g</sup> c<sup>t</sup>  
Ala Arg Val Val Arg Glu Pro Arg Arg Val Leu Arg Glu Met Gly Leu  
130 135 140

g<sup>a</sup> c<sup>t</sup> a<sup>t</sup> t<sup>c</sup> g<sup>a</sup> g<sup>a</sup> a<sup>g</sup> c<sup>t</sup> g<sup>t</sup> a<sup>c</sup> a<sup>t</sup> c<sup>t</sup> c<sup>c</sup> g<sup>t</sup> t<sup>t</sup> g<sup>a</sup> t<sup>t</sup> a<sup>c</sup> a<sup>t</sup> g<sup>c</sup> g<sup>a</sup>  
Glu Leu Ser Glu Ser Val Thr Ile Arg Val Trp Asp Thr Thr Ala Glu  
145 150 155 160

acg cgc ttc ctg gtg ctg ccg ctt ccg ccg ggc gaa acc gaa ggg tgg	528
Thr Arg Phe Leu Val Leu Pro Leu Arg Pro Ala Gly Thr Glu Gly Trp	
165 170 175	
agc gcg gag cag ctc gcg tcg ctc gtc acg cgc gag ggc atg atc ggc	576
Ser Ala Glu Gln Leu Ala Ser Leu Val Thr Arg Glu Ala Met Ile Gly	
180 185 190	
gtg gcg cgg gtc gag gtg gtg tag	600
Val Ala Arg Val Glu Val Val	
195	
<210> 52	
<211> 199	
<212> PRT	
<213> Unknown	
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<223> Metagenome - alpha unit nitrile hydratase - M6dE2	
<400> 52	
Met Ser Asn Pro Arg Arg Arg Glu Arg Ser Ala Pro Pro Asp Ala Arg	
1 5 10 15	
Ala Lys Ala Leu Ala Glu Ala Leu Ser Lys Gln Gly Leu Val Pro Glu	
20 25 30	
Gly Phe Leu Asp Gln Val Gly Ser His Ala Ala Glu Ala Trp Ser Pro	
35 40 45	
Arg Asn Gly Ala Arg Val Val Ala Arg Ala Trp Val Asp Pro Glu Tyr	
50 55 60	
Arg Thr Arg Leu Leu Ala Asp Gly Thr Ala Ala Cys Ala Ala Leu Gly	
65 70 75 80	
Tyr Ala Gly Pro Gln Gly Glu Tyr Ile Val Val Leu Glu Asp Thr Leu	
85 90 95	
Ala Val His Asn Val Ile Val Cys Thr Gln Cys Ser Cys Thr Ala Trp	
100 105 110	
Pro Val Leu Gly Leu Pro Pro Asp Trp Tyr Lys Ser Pro Glu Tyr Arg	
115 120 125	
Ala Arg Val Val Arg Glu Pro Arg Arg Val Leu Arg Glu Met Gly Leu	
130 135 140	
Glu Leu Ser Glu Ser Val Thr Ile Arg Val Trp Asp Thr Thr Ala Glu	
145 150 155 160	
Thr Arg Phe Leu Val Leu Pro Leu Arg Pro Ala Gly Thr Glu Gly Trp	
165 170 175	
Ser Ala Glu Gln Leu Ala Ser Leu Val Thr Arg Glu Ala Met Ile Gly	
180 185 190	

val Ala Arg Val Glu Val Val  
195

<210> 53  
<211> 645  
<212> DNA  
<213> Unknown

<220>  
<223> Metagenome - alpha unit nitrile hydratase - M25A18

<220>  
<221> CDS  
<222> (1)..(645)

<400> 53

atg	agc	ggc	acg	cat	cac	cac	gac	cat	gac	cat	gac	cat	gcc	48		
Met	Ser	Gly	Thr	His	His	His	Asp	His	Asp	His	Asp	His	Asp	Ala		
1				5				10				15				
cat	ccg	ggc	gtc	gcc	aag	gac	gag	aag	gtc	cac	ggc	tat	tac	caa	ttg	96
His	Pro	Gly	Val	Ala	Lys	Asp	Glu	Lys	Val	His	Gly	Tyr	Tyr	Gln	Leu	
				20				25				30				
ctc	ggc	ctc	gcc	atc	aaa	gag	ctg	ctg	atc	gaa	aaa	ggc	gtc	atc	acc	144
Leu	Gly	Leu	Ala	Ile	Lys	Glü	Leu	Leu	Ile	Glu	Lys	Gly	Val	Ile	Thr	
				35			40		45							
gcc	gcc	gag	gtg	cgc	caa	gcg	atc	gag	gcg	cgc	gac	gcg	atc	acg	ccg	192
Ala	Ala	Glu	Val	Arg	Gln	Ala	Ile	Glu	Ala	Arg	Asp	Ala	Ile	Thr	Pro	
				50			55		60							
tcg	ctc	ggc	ggc	aag	gtg	gtc	cgc	cgc	gcc	tgg	acc	gat	ccg	gcc	tac	240
Ser	Leu	Gly	Gly	Lys	Val	Val	Ala	Arg	Ala	Trp	Thr	Asp	Pro	Ala	Tyr	
	65				70				75					80		
aag	gcg	cg	ctg	atc	gcc	gat	ccc	gcc	gcc	atg	atg	gag	atg	ggc	288	
Lys	Ala	Arg	Leu	Ile	Ala	Asp	Pro	Ala	Ala	Ala	Met	Met	Glu	Met	Gly	
				85				90					95			
gtc	gat	ctc	ggc	ccc	acc	gga	ctc	gcc	atc	gcc	gag	aac	acg	ccg	gag	336
Val	Asp	Leu	Gly	Pro	Thr	Gly	Leu	Ala	Ile	Ala	Glu	Asn	Thr	Pro	Glu	
				100			105				110					
gcg	cac	aac	gtc	atc	gtc	tgc	acc	ctg	tgc	tgc	tat	ccg	cgc	gcc	384	
Ala	His	Asn	Val	Ile	Val	Cys	Thr	Leu	Cys	Ser	Cys	Tyr	Pro	Arg	Ala	
				115			120			125						
gtg	ctc	ggc	ctg	ccg	ccc	tcc	tgg	tac	aag	gac	cgc	gat	tac	cg	tcg	432
Val	Leu	Gly	Leu	Pro	Pro	Ser	Trp	Tyr	Lys	Asp	Arg	Asp	Tyr	Arg	Ser	
	130				135			140								
cgc	gtg	gtg	cgc	gag	ccg	cgc	gcc	gtg	ctc	aag	gag	ttc	ggc	acg	gaa	480
Arg	Val	Val	Arg	Glu	Pro	Arg	Ala	Val	Leu	Lys	Glu	Phe	Gly	Thr	Glu	
	145				150				155				160			
ttg	ccc	gac	gac	gtc	gac	gtc	cgc	gtc	cac	gat	tcg	acc	gcc	gat	ctg	528
Leu	Pro	Asp	Asp	Val	Asp	Val	Arg	Val	His	Asp	Ser	Thr	Ala	Asp	Leu	
									165		170		175			
cgc	tat	ctc	gtg	ctg	ccg	atg	cgc	ccg	gcc	ggc	acc	gag	ggc	atg	acg	576
Arg	Tyr	Leu	Val	Leu	Pro	Met	Arg	Pro	Ala	Gly	Thr	Glu	Gly	Met	Ser	
						180		185				190				
gag	gcg	gag	ctg	gcc	gag	atc	gtg	acg	cgc	gac	tgc	atg	atc	ggc	gtg	624
Glu	Ala	Glu	Leu	Ala	Glu	Ile	Val	Thr	Arg	Asp	Cys	Met	Ile	Gly	Val	
						195		200			205					
acg	gtg	ccg	aaa	gcg	ccc	taa									645	

Thr Val Pro Lys Ala Pro  
210

<210> 54  
<211> 214  
<212> PRT  
<213> Unknown

<220>  
<223> Metagenome - alpha unit nitrile hydratase - M25A18

<400> 54

Met Ser Gly Thr His His His Asp His Asp His Asp His Ala  
1 5 10 15

His Pro Gly Val Ala Lys Asp Glu Lys Val His Gly Tyr Tyr Gln Leu  
20 25 30

Leu Gly Leu Ala Ile Lys Glu Leu Leu Ile Glu Lys Gly Val Ile Thr  
35 40 45

Ala Ala Glu Val Arg Gln Ala Ile Glu Ala Arg Asp Ala Ile Thr Pro  
50 55 60

Ser Leu Gly Gly Lys Val Val Ala Arg Ala Trp Thr Asp Pro Ala Tyr  
65 70 75 80

Lys Ala Arg Leu Ile Ala Asp Pro Ala Ala Ala Met Met Glu Met Gly  
85 90 95

Val Asp Leu Gly Pro Thr Gly Leu Ala Ile Ala Glu Asn Thr Pro Glu  
100 105 110

Ala His Asn Val Ile Val Cys Thr Leu Cys Ser Cys Tyr Pro Arg Ala  
115 120 125

Val Leu Gly Leu Pro Pro Ser Trp Tyr Lys Asp Arg Asp Tyr Arg Ser  
130 135 140

Arg Val Val Arg Glu Pro Arg Ala Val Leu Lys Glu Phe Gly Thr Glu  
145 150 155 160

Leu Pro Asp Asp Val Asp Val Arg Val His Asp Ser Thr Ala Asp Leu  
165 170 175

Arg Tyr Leu Val Leu Pro Met Arg Pro Ala Gly Thr Glu Gly Met Ser  
180 185 190

Glu Ala Glu Leu Ala Glu Ile Val Thr Arg Asp Cys Met Ile Gly Val  
195 200 205

Thr Val Pro Lys Ala Pro  
210

<210> 55  
 <211> 627  
 <212> DNA  
 <213> Unknown  
  
 <220>  
 <223> Metagenome - alpha unit nitrile hydratase  
  
 <220>  
 <221> CDS  
 <222> (1)..(627)  
  
 <400> 55

atg	agc	ggt	cac	cat	cac	gac	cac	cat	gag	cac	gac	aac	cac	ttc	48	
Met	Ser	Gly	His	His	His	Asp	His	Asp	His	Glu	His	Asp	Asn	His	Phe	
1			5					10					15			
acg	ccg	atc	gaa	gcg	cgc	gtg	aag	gcg	ctg	gaa	tcg	ctg	ctg	gtc	gcc	96
Thr	Pro	Ile	Glu	Ala	Arg	Val	Lys	Ala	Leu	Glu	Ser	Leu	Leu	Val	Ala	
		20					25						30			
aag	ggc	tat	gtc	gat	ccc	gcc	gcg	ctc	gat	gcg	atc	atc	gac	acc	tat	144
Lys	Gly	Tyr	Val	Asp	Pro	Ala	Ala	Leu	Asp	Ala	Ile	Ile	Asp	Thr	Tyr	
		35				40					45					
gag	acg	aag	atc	ggc	ccg	cgc	aac	ggc	gcc	cgc	gtc	gtc	gcc	aag	gcc	192
Glu	Thr	Lys	Ile	Gly	Pro	Arg	Asn	Gly	Ala	Arg	Val	Val	Ala	Lys	Ala	
		50			55				60							
tgg	acc	gat	ccg	gaa	ttc	gcg	gcg	ctg	aag	cag	gat	ggc	agc	gcc	240	
Trp	Thr	Asp	Pro	Glu	Phe	Ala	Ala	Arg	Leu	Lys	Gln	Asp	Gly	Ser	Ala	
		65			70			75					80			
gcc	gtc	gcc	gaa	ctc	ggc	tat	ggc	ggg	cgt	ggc	ggc	gag	cat	atc	gtc	288
Ala	Val	Ala	Glu	Leu	Gly	Tyr	Gly	Gly	Arg	Gly	Gly	Glu	His	Ile	Val	
		85			90				95							
gcc	tgt	ttc	aat	acg	ccc	gaa	gag	cac	aac	ctg	atc	gtc	tgc	acg	ctc	336
Ala	Cys	Phe	Asn	Thr	Pro	Glu	Glu	His	Asn	Leu	Ile	Val	Cys	Thr	Leu	
		100			105					110						
tgc	tcg	tgc	tat	ccc	tgg	ccg	gtg	ctc	ggc	ctg	ccg	ccg	gtc	tgg	tac	384
Cys	Ser	Cys	Tyr	Pro	Trp	Pro	Val	Leu	Gly	Leu	Pro	Pro	Pro	Val	Trp	Tyr
		115			120			125								
aaa	tcc	ccg	ccc	tat	cgc	tcg	aaa	gcg	gtg	atc	gac	ccg	cgc	ggc	gtg	432
Lys	Ser	Pro	Pro	Tyr	Arg	Ser	Lys	Ala	Val	Ile	Asp	Pro	Arg	Gly	Val	
		130			135			140								
ctg	gcc	gat	ttc	ggc	gtg	acc	ctg	ccg	gag	gga	caa	agg	atc	cgc	gtc	480
Leu	Ala	Asp	Phe	Gly	Val	Thr	Leu	Pro	Glu	Gly	Gln	Arg	Ile	Arg	Val	
		145			150			155			160					
tgg	gat	tcc	acc	gcc	gaa	acc	cgc	ttc	att	gtc	atc	ccc	ctg	cgc	ccg	528
Trp	Asp	Ser	Thr	Ala	Glu	Thr	Arg	Phe	Ile	Val	Ile	Pro	Leu	Arg	Pro	
		165			170			175								
gcc	ggg	acg	gaa	ggc	tgg	tcg	gaa	gaa	cag	ctg	gcg	gcg	atc	gtg	acg	576
Ala	Gly	Thr	Glu	Gly	Trp	Ser	Glu	Glu	Gln	Leu	Ala	Ala	Ile	Val	Thr	
		180			185				190							
cgt	gac	agc	atg	atc	ggc	acc	ggc	gtg	gtc	agc	gcg	gag	gct	tgc	cga	624
Arg	Asp	Ser	Met	Ile	Gly	Thr	Gly	Val	Val	Ser	Ala	Glu	Ala	Ser	Arg	
		195			200			205								
tga															627	

<210> 56  
<211> 208  
<212> PRT  
<213> Unknown

<220>  
<223> Metagenome - alpha unit nitrile hydratase

<400> 56

Met Ser Gly His His His Asp His Asp His Glu His Asp Asn His Phe  
1 5 10 15

Thr Pro Ile Glu Ala Arg Val Lys Ala Leu Glu Ser Leu Leu Val Ala  
20 25 30

Lys Gly Tyr Val Asp Pro Ala Ala Leu Asp Ala Ile Ile Asp Thr Tyr  
35 40 45

Glu Thr Lys Ile Gly Pro Arg Asn Gly Ala Arg Val Val Ala Lys Ala  
50 55 60

Trp Thr Asp Pro Glu Phe Ala Ala Arg Leu Lys Gln Asp Gly Ser Ala  
65 70 75 80

Ala Val Ala Glu Leu Gly Tyr Gly Arg Gly Glu His Ile Val  
85 90 95

Ala Cys Phe Asn Thr Pro Glu Glu His Asn Leu Ile Val Cys Thr Leu  
100 105 110

Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly Leu Pro Pro Val Trp Tyr  
115 120 125

Lys Ser Pro Pro Tyr Arg Ser Lys Ala Val Ile Asp Pro Arg Gly Val  
130 135 140

Leu Ala Asp Phe Gly Val Thr Leu Pro Glu Gly Gln Arg Ile Arg Val  
145 150 155 160

Trp Asp Ser Thr Ala Glu Thr Arg Phe Ile Val Ile Pro Leu Arg Pro  
165 170 175

Ala Gly Thr Glu Gly Trp Ser Glu Glu Gln Leu Ala Ala Ile Val Thr  
180 185 190

Arg Asp Ser Met Ile Gly Thr Gly Val Val Ser Ala Glu Ala Ser Arg  
195 200 205

<210> 57  
 <211> 696  
 <212> DNA  
 <213> Unknown  
  
 <220>  
 <223> Metagenome - alpha unit nitrile hydratase - M3aG10  
  
 <220>  
 <221> CDS  
 <222> (1)..(696)  
  
 <400> 57

atg gat cca acg agg cgt agt ttc ctg gcg tct acc gtt gcc ctg acc	48
Met Asp Pro Thr Arg Arg Ser Phe Leu Ala Ser Thr Val Ala Leu Thr	
1 5 10 15	
gac ggc gca gct atc ccc gat ctg gct cat gcg gca gac cac gac cac	96
Gly Gly Ala Ala Ile Pro Asp Leu Ala His Ala Ala Asp His Asp His	
20 25 30	
cag cat caa gat ttg ccg tcc gat ctg gcg ctg cgg gtg aag tcg ctc	144
Gln His Gln Asp Leu Pro Ser Asp Leu Ala Leu Arg Val Lys Ser Leu	
35 40 45	
gaa tcg ctg ctt gtc gag aag ggg ctg gtg gag cga gca gcg ctc gac	192
Glu Ser Leu Leu Val Glu Lys Gly Leu Val Glu Arg Ala Ala Leu Asp	
50 55 60	
gcg ctg gtg gac acc tac gag cac aaa gtc ggg ccg cga aac gga gcg	240
Ala Leu Val Asp Thr Tyr Glu His Lys Val Gly Pro Arg Asn Gly Ala	
65 70 75 80	
cgc gtt gtc gcg gcc tgg gtt gac ccg gac tac aag caa cgg tta	288
Arg Val Val Ala Arg Ala Trp Val Asp Pro Asp Tyr Lys Gln Arg Leu	
85 90 95	
ttc gcg aac ggt acc gcc gca gtc gcg gag ttc ggc tac tcc ggc tcg	336
Phe Ala Asn Gly Thr Ala Ala Val Ala Glu Phe Gly Tyr Ser Gly Ser	
100 105 110	
cag ggc gct gac atc cgg gtc gtc gaa aac acg gcc act gta cat aac	384
Gln Gly Ala Asp Ile Arg Val Val Glu Asn Thr Ala Thr Val His Asn	
115 120 125	
ctc gtc gtg tgc acg ctg tgc tct tgt tat ccc tgg ccg gtg ctg ggc	432
Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly	
130 135 140	
ttg ccg ccg gtc tgg tac aag tcc gcg ccc tat cgg tct cgc gtg gtg	480
Leu Pro Pro Val Trp Tyr Lys Ser Ala Pro Tyr Arg Ser Arg Val Val	
145 150 155 160	
atc gat ccg cga ggt gtg ctg cgc gag ttc ggc gtg gtg ctg ccg gac	528
Ile Asp Pro Arg Gly Val Leu Arg Glu Phe Gly Val Val Leu Pro Asp	
165 170 175	
cat atc gaa gtg cgt gtc tat gac agc acg gcg gag caa cgc tat cta	576
His Ile Glu Val Arg Val Tyr Asp Ser Thr Ala Glu Gln Arg Tyr Leu	
180 185 190	
gtg ctg ccg gag cgg ccg gcc gga acc gaa aac ctg aca gaa gaa gcg	624
Val Leu Pro Glu Arg Pro Ala Gly Thr Glu Asn Leu Thr Glu Glu Ala	
195 200 205	
ctg gcg ctg ctg gtg acg cgc gac gcg atg att ggc gtg gcc aag gtc	672
Leu Ala Leu Leu Val Thr Arg Asp Ala Met Ile Gly Val Ala Lys Val	
210 215 220	

gcg ccg ccg gga ggc cgc gga tga  
Ala Pro Pro Gly Gly Arg Gly  
225 230

696

<210> 58  
<211> 231  
<212> PRT  
<213> Unknown

<220>  
<223> Metagenome - alpha unit nitrile hydratase - M3aG10

<400> 58

Met Asp Pro Thr Arg Arg Ser Phe Leu Ala Ser Thr Val Ala Leu Thr  
1 5 10 15

Gly Gly Ala Ala Ile Pro Asp Leu Ala His Ala Ala Asp His Asp His  
20 25 30

Gln His Gln Asp Leu Pro Ser Asp Leu Ala Leu Arg Val Lys Ser Leu  
35 40 45

Glu Ser Leu Leu Val Glu Lys Gly Leu Val Glu Arg Ala Ala Leu Asp  
50 55 60

Ala Leu Val Asp Thr Tyr Glu His Lys Val Gly Pro Arg Asn Gly Ala  
65 70 75 80

Arg Val Val Ala Arg Ala Trp Val Asp Pro Asp Tyr Lys Gln Arg Leu  
85 90 95

Phe Ala Asn Gly Thr Ala Ala Val Ala Glu Phe Gly Tyr Ser Gly Ser  
100 105 110

Gln Gly Ala Asp Ile Arg Val Val Glu Asn Thr Ala Thr Val His Asn  
115 120 125

Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly  
130 135 140

Leu Pro Pro Val Trp Tyr Lys Ser Ala Pro Tyr Arg Ser Arg Val Val  
145 150 155 160

Ile Asp Pro Arg Gly Val Leu Arg Glu Phe Gly Val Val Leu Pro Asp  
165 170 175

His Ile Glu Val Arg Val Tyr Asp Ser Thr Ala Glu Gln Arg Tyr Leu  
180 185 190

Val Leu Pro Glu Arg Pro Ala Gly Thr Glu Asn Leu Thr Glu Glu Ala  
195 200 205

Leu Ala Leu Leu Val Thr Arg Asp Ala Met Ile Gly Val Ala Lys Val  
210 215 220

Ala Pro Pro Gly Gly Arg Gly  
225 230

<210> 59  
<211> 609  
<212> DNA  
<213> Unknown

<220>  
<223> Metagenome - alpha unit nitrile hydratase - M73dc9

<220>  
<221> CDS  
<222> (1)..(609)

<400> 59

atg	agc	tcg	aag	ccc	acc	gaa	gat	ctc	ggc	acc	tac	cag	ccg	ctc	acc	48
Met	Ser	Ser	Lys	Pro	Thr	Glu	Asp	Leu	Gly	Thr	Tyr	Gln	Pro	Leu	Thr	
1				5				10				15				
tac	tac	cag	atg	atg	gaa	gtg	agc	ctg	cgc	gag	ctg	ctg	gtg	gag	aag	96
Tyr	Tyr	Gln	Met	Met	Glu	Val	Ser	Leu	Arg	Glu	Leu	Leu	Val	Glu	Lys	
20				25				25				30				
ggc	gtg	atc	acc	gaa	gcg	gaa	gtc	gcc	cgc	gcg	atg	ggc	gag	atc	ggc	144
Gly	Val	Ile	Thr	Glu	Ala	Glu	Val	Ala	Arg	Ala	Met	Gly	Glu	Ile	Gly	
35				40				40			45					
gcg	aga	agc	ccg	gag	cgc	ggc	gcg	aag	atg	gtc	gcg	cgc	gcg	tgg	gtg	192
Ala	Arg	Ser	Pro	Glu	Arg	Gly	Ala	Lys	Met	Val	Ala	Arg	Ala	Trp	Val	
50				55				55			60					
gac	ccg	gcf	tac	aag	gcf	cgc	atg	ctt	gcc	gac	ggc	agc	aag	gcc	gcc	240
Asp	Pro	Ala	Tyr	Lys	Ala	Arg	Met	Leu	Ala	Asp	Gly	Ser	Lys	Ala	Ala	
65				70				70			75					
gag	gag	ctc	ggg	tcc	gag	gtg	ccg	ggc	ctc	aag	ctg	atc	gtg	gtc	gag	288
Glu	Glu	Leu	Gly	Phe	Glu	Val	Pro	Gly	Leu	Lys	Leu	Ile	Val	Val	Glu	
85					90				90			95				
aac	acc	gcf	gac	acg	cac	aac	gtg	gtc	gtg	acg	ctg	tgc	tgc	tgc	tgc	336
Asn	Thr	Ala	Asp	Thr	His	Asn	Val	Val	Val	Cys	Thr	Leu	Cys	Ser	Cys	
100						105					110					
tac	ccg	cgc	atc	ctg	ctc	ggc	atc	ccg	ccc	gag	tgg	tac	aag	tgc	cgc	384
Tyr	Pro	Arg	Ile	Leu	Leu	Gly	Ile	Pro	Pro	Glu	Trp	Tyr	Lys	Ser	Arg	
115						120					125					
agc	tac	cgc	agc	cgc	aca	gtg	cgc	gag	ccg	cgc	gcf	gtg	ctc	gcc	gaa	432
Ser	Tyr	Arg	Ser	Arg	Thr	Val	Arg	Glu	Pro	Arg	Ala	Val	Leu	Ala	Glu	
130						135					140					
tcc	ggc	acg	acc	atc	ccg	gag	aac	gtc	gcf	atc	cga	gtg	cac	gac	agc	480
Phe	Gly	Thr	Thr	Ile	Pro	Glu	Asn	Val	Ala	Ile	Arg	Val	His	Asp	Ser	
145						150					155			160		
act	gcf	gac	atg	cgc	tac	ctc	gtg	atg	ccg	atg	cgg	cct	gcf	ggc	acc	528
Thr	Ala	Asp	Met	Arg	Tyr	Leu	Val	Met	Pro	Met	Arg	Pro	Ala	Gly	Thr	
165								165			170			175		
gaa	aat	tcc	acc	gaa	gag	cag	ctc	gct	gca	ttg	gtg	acg	cgc	gac	agc	576
Glu	Asn	Phe	Thr	Glu	Glu	Gln	Leu	Ala	Ala	Leu	Val	Thr	Arg	Asp	Ser	
180								180			185			190		
ctg	atc	ggf	gtt	tcc	tta	gca	acg	ctt	ccg	tag						609
Leu	Ile	Gly	Val	Ser	Leu	Ala	Thr	Leu	Pro							
195								195			200					

<210> 60  
<211> 202  
<212> PRT  
<213> Unknown

<220>

<223> Metagenome - alpha unit nitrile hydratase - M73dc9

<400> 60

Met Ser Ser Lys Pro Thr Glu Asp Leu Gly Thr Tyr Gln Pro Leu Thr  
1 5 10 15

Tyr Tyr Gln Met Met Glu Val Ser Leu Arg Glu Leu Leu Val Glu Lys  
20 25 30

Gly Val Ile Thr Glu Ala Glu Val Ala Arg Ala Met Gly Glu Ile Gly  
35 40 45

Ala Arg Ser Pro Glu Arg Gly Ala Lys Met Val Ala Arg Ala Trp Val  
50 55 60

Asp Pro Ala Tyr Lys Ala Arg Met Leu Ala Asp Gly Ser Lys Ala Ala  
65 70 75 80

Glu Glu Leu Gly Phe Glu Val Pro Gly Leu Lys Leu Ile Val Val Glu  
85 90 95

Asn Thr Ala Asp Thr His Asn Val Val Val Cys Thr Leu Cys Ser Cys  
100 105 110

Tyr Pro Arg Ile Leu Leu Gly Ile Pro Pro Glu Trp Tyr Lys Ser Arg  
115 120 125

Ser Tyr Arg Ser Arg Thr Val Arg Glu Pro Arg Ala Val Leu Ala Glu  
130 135 140

Phe Gly Thr Thr Ile Pro Glu Asn Val Ala Ile Arg Val His Asp Ser  
145 150 155 160

Thr Ala Asp Met Arg Tyr Leu Val Met Pro Met Arg Pro Ala Gly Thr  
165 170 175

Glu Asn Phe Thr Glu Glu Gln Leu Ala Ala Leu Val Thr Arg Asp Ser  
180 185 190

Leu Ile Gly Val Ser Leu Ala Thr Leu Pro  
195 200

<210> 61  
 <211> 825  
 <212> DNA  
 <213> Unknown  
  
 <220>  
 <223> Metagenome - beta unit nitrile hydratase  
  
 <220>  
 <221> CDS  
 <222> (1)..(825)  
  
 <400> 61

atg	gtg	gga	cgt	ggg	aag	tgg	gca	ctt	ggc	agt	agg	cag	ttt	gct	gcg		48
Met	Val	Gly	Arg	Gly	Lys	Trp	Ala	Leu	Gly	Ser	Arg	Gln	Phe	Ala	Ala		
1									10					15			
gct	gcc	aac	tgg	caa	ctt	atc	agt	cgc	cct	tca	tgg	tca	gct	tgt	aat		96
Ala	Ala	Asn	Trp	Gln	Leu	Ile	Ser	Arg	Pro	Ser	Trp	Ser	Ala	Cys	Asn		
						20			25				30				
ata	ttg	gtc	ctc	atg	agc	gcc	acg	cac	ccc	aaa	aag	cgc	gcc	gcc	gac		144
Ile	Leu	Val	Leu	Met	Ser	Ala	Thr	His	Pro	Lys	Lys	Arg	Ala	Ala	Asp		
						35			40			45					
atc	ggc	ggc	aac	aaa	gcc	ggc	gtg	gac	acc	gcg	gat	cac	ggc	atg		192	
Ile	Gly	Gly	Asn	Lys	Ala	Gly	Ala	Val	Asp	Thr	Ala	Asp	His	Gly	Met		
						50			55			60					
aag	ttc	tgg	gag	cgg	cag	gcc	aac	gcc	ctg	cgc	acc	gcg	ctg	cgg	cgc		240
Lys	Phe	Trp	Glu	Arg	Gln	Ala	Asn	Ala	Leu	Arg	Thr	Ala	Leu	Arg	Arg		
						65			70			75			80		
aat	gga	ctg	atg	agc	gta	gat	gag	ctg	cgc	cgc	gca	gcg	gag	gac	ctg		288
Asn	Gly	Leu	Met	Ser	Val	Asp	Glu	Leu	Arg	Arg	Ala	Ala	Glu	Asp	Leu		
						85			90				95				
gga	gac	cgc	tac	gcg	aag	ctt	gag	tac	ttc	gag	cgc	acg	acg	ttc	gcg		336
Gly	Asp	Arg	Tyr	Ala	Lys	Leu	Glu	Tyr	Phe	Glu	Arg	Thr	Thr	Phe	Ala		
						100			105				110				
ctg	cgc	acg	gtc	ctg	ctc	gaa	aag	ggc	tac	ttc	acg	gag	gag	tcg	ctc		384
Leu	Arg	Thr	Val	Leu	Leu	Glu	Lys	Gly	Tyr	Phe	Thr	Glu	Glu	Ser	Leu		
						115			120				125				
gcg	gcg	aag	atg	gcc	gag	gtg	cgg	aag	ccg	ctt	cga	tgt	gcc	gcg	caa		432
Ala	Ala	Lys	Met	Ala	Glu	Val	Arg	Lys	Pro	Leu	Arg	Cys	Ala	Ala	Gln		
						130			135			140					
gaa	gga	att	gcc	ggt	gaa	gaa	gaa	agt	gaa	gct	atg	aac	cca	gct	acg		480
Glu	Gly	Ile	Ala	Gly	Glu	Glu	Glu	Ser	Glu	Ala	Met	Asn	Pro	Ala	Thr		
						145			150			155			160		
ggc	aag	cag	gac	ggc	caa	cgg	ctg	cca	tct	acg	tat	acc	gct	gct	ccc		528
Gly	Lys	Gln	Asp	Gly	Gln	Arg	Leu	Pro	Ser	Thr	Tyr	Thr	Ala	Ala	Pro		
						165			170				175				
ggg	cac	cga	ttc	gat	gtc	ggt	gac	cgc	gtt	gtg	gtc	aag	cgc	tca	aat		576
Gly	His	Arg	Phe	Asp	Val	Gly	Asp	Arg	Val	Val	Val	Lys	Arg	Ser	Asn		
						180			185				190				
ccg	ccc	ggc	cac	cgc	cgc	acg	cct	cat	tac	atc	cgc	ggc	aag	acg	ggc		624
Pro	Pro	Gly	His	Arg	Arg	Thr	Pro	His	Tyr	Ile	Arg	Gly	Lys	Thr	Gly		
						195			200			205					
gtg	atc	gag	cgc	atc	tgc	ggc	gcc	ttc	ccc	aac	ccg	gaa	gag	ctg	gca		672
Val	Ile	Glu	Arg	Ile	Cys	Gly	Ala	Phe	Pro	Asn	Pro	Glu	Glu	Leu	Ala		
						210			215			220					

tac gga ttc gac ggc gaa ccg aag aag gtg ctc tac cgc gtg cga ttc	720
Tyr Gly Phe Asp Gly Glu Pro Lys Lys Val Leu Tyr Arg Val Arg Phe	
225 230 235 240	
cgg caa aaa gag gtg tgg ccg gcc tat cgc ggc ccg gcg cac gac gtg	768
Arg Gln Lys Glu Val Trp Pro Ala Tyr Arg Gly Pro Ala His Asp Val	
245 250 255	
atc gag atg gag att ttc gag cat tgg ctc gag ccg gcg cag agc cag	816
Ile Glu Met Glu Ile Phe Glu His Trp Leu Glu Pro Ala Gln Ser Gln	
260 265 270	
aaa acc tga	825
Lys Thr	

<210> 62  
 <211> 274  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Metagenome - beta unit nitrile hydratase

<400> 62

Met Val Gly Arg Gly Lys Trp Ala Leu Gly Ser Arg Gln Phe Ala Ala  
 1 5 10 15

Ala Ala Asn Trp Gln Leu Ile Ser Arg Pro Ser Trp Ser Ala Cys Asn  
 20 25 30

Ile Leu Val Leu Met Ser Ala Thr His Pro Lys Lys Arg Ala Ala Asp  
 35 40 45

Ile Gly Gly Asn Lys Ala Gly Ala Val Asp Thr Ala Asp His Gly Met  
 50 55 60

Lys Phe Trp Glu Arg Gln Ala Asn Ala Leu Arg Thr Ala Leu Arg Arg  
 65 70 75 80

Asn Gly Leu Met Ser Val Asp Glu Leu Arg Arg Ala Ala Glu Asp Leu  
 85 90 95

Gly Asp Arg Tyr Ala Lys Leu Glu Tyr Phe Glu Arg Thr Thr Phe Ala  
 100 105 110

Leu Arg Thr Val Leu Leu Glu Lys Gly Tyr Phe Thr Glu Glu Ser Leu  
 115 120 125

Ala Ala Lys Met Ala Glu Val Arg Lys Pro Leu Arg Cys Ala Ala Gln  
 130 135 140

Glu Gly Ile Ala Gly Glu Glu Glu Ser Glu Ala Met Asn Pro Ala Thr  
 145 150 155 160

Gly Lys Gln Asp Gly Gln Arg Leu Pro Ser Thr Tyr Thr Ala Ala Pro  
 165 170 175

Gly His Arg Phe Asp Val Gly Asp Arg Val Val Val Lys Arg Ser Asn  
 180 185 190  
 Pro Pro Gly His Arg Arg Thr Pro His Tyr Ile Arg Gly Lys Thr Gly  
 195 200 205  
 Val Ile Glu Arg Ile Cys Gly Ala Phe Pro Asn Pro Glu Glu Leu Ala  
 210 215 220  
 Tyr Gly Phe Asp Gly Glu Pro Lys Lys Val Leu Tyr Arg Val Arg Phe  
 225 230 235 240  
 Arg Gln Lys Glu Val Trp Pro Ala Tyr Arg Gly Pro Ala His Asp Val  
 245 250 255  
 Ile Glu Met Glu Ile Phe Glu His Trp Leu Glu Pro Ala Gln Ser Gln  
 260 265 270  
 Lys Thr

<210> 63  
 <211> 627  
 <212> DNA  
 <213> Unknown  
 <220>  
 <223> Metagenome - beta unit nitrile hydratase - M12K24  
 <220>  
 <221> CDS  
 <222> (1)..(627)  
 <400> 63

atg gac ggc atg cac gac ctg gga ggc agg cag ggc ttc gga ccc gtt	48
Met Asp Gly Met His Asp Leu Gly Gly Arg Gln Gly Phe Gly Pro Val	
1 5 10 15	
cgc tac acg atc gac gcg ccc gca ttc cat tcg ccg tgg gaa gtg cgc	96
Arg Tyr Thr Ile Asp Ala Pro Ala Phe His Ser Pro Trp Glu Val Arg	
20 25 30	
gcg aat tcg ctc tat gcg ttc gcg gtg cgc ctc ggc atc ttc aac atg	144
Ala Asn Ser Leu Tyr Ala Phe Ala Val Arg Leu Gly Ile Phe Asn Met	
35 40 45	
gac gaa tac cgc cat gcg atc gag cgg atg gag ccg cgc cat tac ctc	192
Asp Glu Tyr Arg His Ala Ile Glu Arg Met Glu Pro Arg His Tyr Leu	
50 55 60	
ggc gcc ggc tat tac gaa cgc tcg ttg acc ggc ctc gcg acc ttg ctg	240
Gly Ala Gly Tyr Tyr Glu Arg Ser Leu Thr Gly Leu Ala Thr Leu Leu	
65 70 75 80	
gtc gag aag ggc gtc gtg acg cgc gag gaa ctc gag acc cgg gcg cag	288
Val Glu Lys Gly Val Val Thr Arg Glu Glu Leu Glu Thr Arg Ala Gln	
85 90 95	
ggc cgc tac ccg ctg gcg atg ccc agc gcg cct ggc cgc acc aat gcg	336
Gly Arg Tyr Pro Leu Ala Met Pro Ser Ala Pro Gly Arg Thr Asn Ala	
100 105 110	

cag gca cgc gag cgt ttc cag ccg ggc gac cgg gtt cgc gtc aag gcg Gln Ala Arg Glu Arg Phe Gln Pro Gly Asp Arg Val Arg Val Lys Ala 115 120 125	384
gat ttc gtg tcg ggg cac gtg cgg atg ccg gcg tac atc cgc ggc aag Asp Phe Val Ser Gly His Val Arg Met Pro Ala Tyr Ile Arg Gly Lys 130 135 140	432
acc ggc gtg gtc gtc agc gag tcc ccg gac tat ccg ttt ccc gat gcg Thr Gly Val Val Val Ser Glu Ser Pro Asp Tyr Pro Phe Pro Asp Ala 145 150 155 160	480
cat gcg cac tcg gtc gat gcc cag gac gag cca acc tac gac gtg cgc His Ala His Ser Val Asp Ala Gln Asp Glu Pro Thr Tyr Asp Val Arg 165 170 175	528
ttc cgc agc gag gat cta tgg ccg gat tcc gcc gat tcc gca ctc gtt Phe Arg Ser Glu Asp Leu Trp Pro Asp Ser Ala Asp Ser Ala Leu Val 180 185 190	576
cac gtc ggc gta ttc cag agc tac ctc gag cgg gag tcg acg cca gga His Val Gly Val Phe Gln Ser Tyr Leu Glu Arg Glu Ser Thr Pro Gly 195 200 205	624
tag	627

<210> 64  
<211> 208  
<212> PRT  
<213> Unknown

<220>  
<223> Metagenome - beta unit nitrile hydratase - M12K24

<400> 64

Met Asp Gly Met His Asp Leu Gly Gly Arg Gln Gly Phe Gly Pro Val  
1 5 10 15

Arg Tyr Thr Ile Asp Ala Pro Ala Phe His Ser Pro Trp Glu Val Arg  
20 25 30

Ala Asn Ser Leu Tyr Ala Phe Ala Val Arg Leu Gly Ile Phe Asn Met  
35 40 45

Asp Glu Tyr Arg His Ala Ile Glu Arg Met Glu Pro Arg His Tyr Leu  
50 55 60

Gly Ala Gly Tyr Tyr Glu Arg Ser Leu Thr Gly Leu Ala Thr Leu Leu  
65 70 75 80

Val Glu Lys Gly Val Val Thr Arg Glu Glu Leu Glu Thr Arg Ala Gln  
85 90 95

Gly Arg Tyr Pro Leu Ala Met Pro Ser Ala Pro Gly Arg Thr Asn Ala  
100 105 110

Gln Ala Arg Glu Arg Phe Gln Pro Gly Asp Arg Val Arg Val Lys Ala  
115 120 125

Asp Phe Val Ser Gly His Val Arg Met Pro Ala Tyr Ile Arg Gly Lys  
130 135 140

Thr Gly Val Val Val Ser Glu Ser Pro Asp Tyr Pro Phe Pro Asp Ala  
145 150 155 160

His Ala His Ser Val Asp Ala Gln Asp Glu Pro Thr Tyr Asp Val Arg  
165 170 175

Phe Arg Ser Glu Asp Leu Trp Pro Asp Ser Ala Asp Ser Ala Leu Val  
180 185 190

His Val Gly Val Phe Gln Ser Tyr Leu Glu Arg Glu Ser Thr Pro Gly  
195 200 205

<210> 65

<211> 660

<212> DNA

<213> Unknown

<220>

<223> Metagenome - beta unit nitrile hydratase - M29M24

<220>

<221> CDS

<222> (1)..(660)

<400> 65

atg aac ggc gtt cat gac atg ggc ggc atg cac ggc atg ggt gcg atc 48  
Met Asn Gly Val His Asp Met Gly Gly Met His Gly Met Gly Ala Ile  
1 5 10 15

cgc cgc gag gag aac gag ccc gct ttc cac gag ccc tgg gag ggg cgg 96  
Arg Arg Glu Glu Asn Glu Pro Ala Phe His Glu Pro Trp Glu Gly Arg  
20 25 30

gtt ttc gct ctg acc acg gcg gtc gag gcc tgg ggt cgg tgg acc ctc 144  
Val Phe Ala Leu Thr Thr Ala Val Glu Ala Trp Gly Arg Trp Thr Leu  
35 40 45

gat gct tcc cga cac cgg atc gag cgg atg aat gcg gcg gac tat ctg 192  
Asp Ala Ser Arg His Arg Ile Glu Arg Met Asn Ala Ala Asp Tyr Leu  
50 55 60

cgg gtg agc tat tac gag aag tgg ctc gag tcg ctt ctc gct ctc ctg 240  
Arg Val Ser Tyr Tyr Glu Lys Trp Leu Glu Ser Leu Leu Ala Leu Leu  
65 70 75 80

tcc gag acc gga atg gcg agt ccg gcg gag ata cgg agt ggg gag cgt 288  
Ser Glu Thr Gly Met Ala Ser Pro Ala Glu Ile Arg Ser Gly Glu Arg  
85 90 95

gcc gac ggc aca ccg aaa gcg acc ccg ccg ctc ccg gcc gac cac gtg 336  
Ala Asp Gly Thr Pro Lys Ala Thr Pro Leu Pro Ala Asp His Val  
100 105 110

acg gcg att ctc gcc agc ggg ttt ccc gcg agc cgg gag gcg gga gct 384  
Thr Ala Ile Leu Ala Ser Gly Phe Pro Ala Ser Arg Glu Ala Gly Ala  
115 120 125

gcg cct cgc ttc cga gtg agc gag cgg gtg cgc acc cgg aac atc aac 432  
Ala Pro Arg Phe Arg Val Ser Glu Arg Val Arg Thr Arg Asn Ile Asn  
130 135 140

ccg acg act cac acg cgc ctt ccg cga tac gcc cgg cgg aag ctc ggg 480  
Pro Thr Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Arg Lys Leu Gly  
145 150 155 160

acg atc gag cgc gac cac gga gtc ttc gtc ttc ccg gat acg aac gcg	528
Thr Ile Glu Arg Asp His Gly Val Phe Val Phe Pro Asp Thr Asn Ala	
165 170 175	
cac gct ctc ggg gag aaa ccg cag cac gtc tat tcg gtt cgt ttc gag	576
His Ala Leu Gly Glu Lys Pro Gln His Val Tyr Ser Val Arg Phe Glu	
180 185 190	
gcg cgt gag ctc tgg ggc gag act gcc agg cca gag gat tcc gtc tac	624
Ala Arg Glu Leu Trp Gly Glu Thr Ala Arg Pro Glu Asp Ser Val Tyr	
195 200 205	
atc gat ctt tgg gac gag tac ctt gaa ccc gtg tag	660
Ile Asp Leu Trp Asp Glu Tyr Leu Glu Pro Val	
210 215	
<210> 66	
<211> 219	
<212> PRT	
<213> Unknown	
<220>	
<223> Metagenome - beta unit nitrile hydratase - M29M24	
<400> 66	
Met Asn Gly Val His Asp Met Gly Gly Met His Gly Met Gly Ala Ile	
1 5 10 15	
Arg Arg Glu Glu Asn Glu Pro Ala Phe His Glu Pro Trp Glu Gly Arg	
20 25 30	
Val Phe Ala Leu Thr Thr Ala Val Glu Ala Trp Gly Arg Trp Thr Leu	
35 40 45	
Asp Ala Ser Arg His Arg Ile Glu Arg Met Asn Ala Ala Asp Tyr Leu	
50 55 60	
Arg Val Ser Tyr Tyr Glu Lys Trp Leu Glu Ser Leu Leu Ala Leu Leu	
65 70 75 80	
Ser Glu Thr Gly Met Ala Ser Pro Ala Glu Ile Arg Ser Gly Glu Arg	
85 90 95	
Ala Asp Gly Thr Pro Lys Ala Thr Pro Pro Leu Pro Ala Asp His Val	
100 105 110	
Thr Ala Ile Leu Ala Ser Gly Phe Pro Ala Ser Arg Glu Ala Gly Ala	
115 120 125	
Ala Pro Arg Phe Arg Val Ser Glu Arg Val Arg Thr Arg Asn Ile Asn	
130 135 140	
Pro Thr Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Arg Lys Leu Gly	
145 150 155 160	
Thr Ile Glu Arg Asp His Gly Val Phe Val Phe Pro Asp Thr Asn Ala	
165 170 175	

His Ala Leu Gly Glu Lys Pro Gln His Val Tyr Ser Val Arg Phe Glu  
180 185 190

Ala Arg Glu Leu Trp Gly Glu Thr Ala Arg Pro Glu Asp Ser Val Tyr  
195 200 205

Ile Asp Leu Trp Asp Glu Tyr Leu Glu Pro Val  
210 215

<210> 67  
<211> 660  
<212> DNA  
<213> Unknown

<220>  
<223> Metagenome - beta unit nitrile hydratase - M2K17

<220>  
<221> CDS  
<222> (1)..(660)

<400> 67

atg acc aat tcg ctg cac gac atg ggc ggc atg cac ggc ttt ggc cgg Met Thr Asn Ser Leu His Asp Met Gly Gly Met His Gly Phe Gly Arg	48
1 5 10 15	
gtc gag ccc gag ccg aac gag ccg ccg ttt cac cag cgc tgg gag ggc Val Glu Pro Glu Pro Asn Glu Pro Pro Phe His Gln Arg Trp Glu Gly	96
20 25 30	
cgg gtg ctg ggg atg cag cgc gcc atg ggc ttt acc ggg ctg tgg acc Arg Val Leu Gly Met Gln Arg Ala Met Gly Phe Thr Gly Leu Trp Thr	144
35 40 45	
atc gac gcc ggc cgc gcc tcg ctc gaa gcc ctg ccg cca tta gcg tat Ile Asp Ala Gly Arg Ala Ser Leu Glu Ala Leu Pro Pro Leu Ala Tyr	192
50 55 60	
ctg ggt tcg tcc tac tat cgg cgc tgg ttt ctt ggc ctg gag agc cgg Leu Gly Ser Ser Tyr Tyr Arg Arg Trp Phe Leu Gly Leu Glu Ser Arg	240
65 70 75 80	
ctg ctg ctg cgc ggc ctc gtt ggc gag gac gag atc gcg gca ggc cgt Leu Leu Leu Arg Gly Leu Val Gly Glu Asp Glu Ile Ala Ala Gly Arg	288
85 90 95	
tcg atg cgc gcc ggc gcc atg ttg ccg cgc acc ctg acc cag gcc gat Ser Met Arg Ala Gly Ala Met Leu Pro Arg Thr Leu Thr Gln Ala Asp	336
100 105 110	
gtg gag aaa acc ctg acc cgc ggc gac ttc gcc cgc ccg acc aac acc Val Glu Lys Thr Leu Thr Arg Gly Asp Phe Ala Arg Pro Thr Asn Thr	384
115 120 125	
ccg gcg cgt ttc cag ccg ggc gac cgg gtg caa acg aag aac atc aac Pro Ala Arg Phe Gln Pro Gly Asp Arg Val Gln Thr Lys Asn Ile Asn	432
130 135 140	
ccg gcg acc cac acc cgc ctg ccg cgc tat gcc cgc ggc aag act ggc Pro Ala Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly Lys Thr Gly	480
145 150 155 160	
acg gtc gag gcg gtc cgc ggc gtt cac gtc ttt ccc gac acc gcc gcg Thr Val Glu Ala Val Arg Gly Val His Val Phe Pro Asp Thr Ala Ala	528
165 170 175	

ctc ggc gcc ggc gac gac ccg caa tgg ctc tac gcc gtg gtc ttc ccg	576
Leu Gly Ala Gly Asp Asp Pro Gln Trp Leu Tyr Ala Val Val Phe Pro	
180 185 190	
gcg cgc gag ttg tgg gga gag gcg gcc gat ccc gcg atc aaa atc tcg	624
Ala Arg Glu Leu Trp Gly Glu Ala Ala Asp Pro Ala Ile Lys Ile Ser	
195 200 205	
atc gag gcg ttc gaa ccc tat atc gac ccc gca tga	660
Ile Glu Ala Phe Glu Pro Tyr Ile Asp Pro Ala	
210 215	
<210> 68	
<211> 219	
<212> PRT	
<213> Unknown	
<220>	
<223> Metagenome - beta unit nitrile hydratase - M2K17	
<400> 68	
Met Thr Asn Ser Leu His Asp Met Gly Gly Met His Gly Phe Gly Arg	
1 5 10 15	
Val Glu Pro Glu Pro Asn Glu Pro Pro Phe His Gln Arg Trp Glu Gly	
20 25 30	
Arg Val Leu Gly Met Gln Arg Ala Met Gly Phe Thr Gly Leu Trp Thr	
35 40 45	
Ile Asp Ala Gly Arg Ala Ser Leu Glu Ala Leu Pro Pro Leu Ala Tyr	
50 55 60	
Leu Gly Ser Ser Tyr Tyr Arg Arg Trp Phe Leu Gly Leu Glu Ser Arg	
65 70 75 80	
Leu Leu Leu Arg Gly Leu Val Gly Glu Asp Glu Ile Ala Ala Gly Arg	
85 90 95	
Ser Met Arg Ala Gly Ala Met Leu Pro Arg Thr Leu Thr Gln Ala Asp	
100 105 110	
Val Glu Lys Thr Leu Thr Arg Gly Asp Phe Ala Arg Pro Thr Asn Thr	
115 120 125	
Pro Ala Arg Phe Gln Pro Gly Asp Arg Val Gln Thr Lys Asn Ile Asn	
130 135 140	
Pro Ala Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly Lys Thr Gly	
145 150 155 160	
Thr Val Glu Ala Val Arg Gly Val His Val Phe Pro Asp Thr Ala Ala	
165 170 175	
Leu Gly Ala Gly Asp Asp Pro Gln Trp Leu Tyr Ala Val Val Phe Pro	
180 185 190	

Ala Arg Glu Leu Trp Gly Glu Ala Ala Asp Pro Ala Ile Lys Ile Ser  
195 200 205

Ile Glu Ala Phe Glu Pro Tyr Ile Asp Pro Ala  
210 215

<210> 69  
<211> 663  
<212> DNA  
<213> Unknown

<220>  
<223> Metagenome - beta unit nitrile hydratase - M23dA12

<220>  
<221> CDS  
<222> (1)..(663)

<400> 69

atg gac ggc gtg cac gac atg ggc ggc atg cac ggt ttc ggc aag gtc Met Asp Gly Val His Asp Met Gly Gly Met His Gly Phe Gly Lys Val	48
1 5 10 15	
gag ccg gaa gcg aac gag ccc gcc ttc cat gcg gaa tgg gaa ggc cgc Glu Pro Glu Ala Asn Glu Pro Ala Phe His Ala Glu Trp Glu Gly Arg	96
20 25 30	
tgc ctc gcg ctc aac cgc gcc atg ggt gcg atc ggc gcc tgg acc atc Cys Leu Ala Leu Asn Arg Ala Met Gly Ala Ile Gly Ala Trp Thr Ile	144
35 40 45	
gat gaa ggc cgt gcc ggc atc gag atc ctg ccg ccg gag att tat ctt Asp Glu Gly Arg Ala Gly Ile Glu Ile Leu Pro Pro Glu Ile Tyr Leu	192
50 55 60	
ggc agt tcg tac tat gga aaa tgg gcg cgg ctg gag aat atg gtg Gly Ser Ser Tyr Tyr Gly Lys Trp Ala Arg Arg Leu Glu Asn Met Val	240
65 70 75 80	
gtc gca cgc ggg ttc gcg ggc gcc gat gaa ctc gcc gcg ggt cgc gca Val Ala Arg Gly Phe Ala Gly Ala Asp Glu Leu Ala Ala Gly Arg Ala	288
85 90 95	
gcg cgt ccc ggc aga tcg gtg aaa cga aag ctt acg gtc gcc gaa gtg Ala Arg Pro Gly Arg Ser Val Lys Arg Lys Leu Thr Val Ala Glu Val	336
100 105 110	
ccg cgc acg ctg acg cgc ggt tca ttt ttc cgc gag gca aca aag ccg Pro Arg Thr Leu Thr Arg Gly Ser Phe Phe Arg Glu Ala Thr Lys Pro	384
115 120 125	
gca cga ttt gcg gtc ggc gaa cgc gtg cgc acc agg aac att cat ccg Ala Arg Phe Ala Val Gly Glu Arg Val Arg Thr Arg Asn Ile His Pro	432
130 135 140	
gcg acg cac act cgg ttg ccg cga tat gcg cgc ggc cat gtc ggc gtg Ala Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly His Val Gly Val	480
145 150 155 160	
atc gag gcg atc cgc ggt tgc cac gta ttt ccc gac tcg gtt gcg atc Ile Glu Ala Ile Arg Gly Cys His Val Phe Pro Asp Ser Val Ala Ile	528
165 170 175	
ggc gcc ggc gag aac ccg caa tgg ctt tat acg gtg gtg ttc gaa ggc Gly Ala Gly Glu Asn Pro Gln Trp Leu Tyr Thr Val Val Phe Glu Gly	576
180 185 190	

cgc acg ctg tgg ggc gat agc gcc gat ccg acg ctt aag gtc tcg atc	624
Arg Thr Leu Trp Gly Asp Ser Ala Asp Pro Thr Leu Lys Val Ser Ile	
195 200 205	
gag gcg ttc gag ccg tat ctg gaa ccg gcc caa cca tga	663
Glu Ala Phe Glu Pro Tyr Leu Glu Pro Ala Gln Pro	
210 215 220	
<210> 70	
<211> 220	
<212> PRT	
<213> Unknown	
<220>	
<223> Metagenome - beta unit nitrile hydratase - M23dA12	
<400> 70	
Met Asp Gly Val His Asp Met Gly Gly Met His Gly Phe Gly Lys Val	
1 5 10 15	
Glu Pro Glu Ala Asn Glu Pro Ala Phe His Ala Glu Trp Glu Gly Arg	
20 25 30	
Cys Leu Ala Leu Asn Arg Ala Met Gly Ala Ile Gly Ala Trp Thr Ile	
35 40 45	
Asp Glu Gly Arg Ala Gly Ile Glu Ile Leu Pro Pro Glu Ile Tyr Leu	
50 55 60	
Gly Ser Ser Tyr Tyr Gly Lys Trp Ala Arg Arg Leu Glu Asn Met Val	
65 70 75 80	
Val Ala Arg Gly Phe Ala Gly Ala Asp Glu Leu Ala Ala Gly Arg Ala	
85 90 95	
Ala Arg Pro Gly Arg Ser Val Lys Arg Lys Leu Thr Val Ala Glu Val	
100 105 110	
Pro Arg Thr Leu Thr Arg Gly Ser Phe Phe Arg Glu Ala Thr Lys Pro	
115 120 125	
Ala Arg Phe Ala Val Gly Glu Arg Val Arg Thr Arg Asn Ile His Pro	
130 135 140	
Ala Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly His Val Gly Val	
145 150 155 160	
Ile Glu Ala Ile Arg Gly Cys His Val Phe Pro Asp Ser Val Ala Ile	
165 170 175	
Gly Ala Gly Glu Asn Pro Gln Trp Leu Tyr Thr Val Val Phe Glu Gly	
180 185 190	
Arg Thr Leu Trp Gly Asp Ser Ala Asp Pro Thr Leu Lys Val Ser Ile	
195 200 205	

Glu	Ala	Phe	Glu	Pro	Tyr	Leu	Glu	Pro	Ala	Gln	Pro					
210						215						220				
<210> 71																
<211> 888																
<212> DNA																
<213> Unknown																
<220>																
<223> Metagenome - beta unit nitrile hydratase - M49bd9																
<220>																
<221> CDS																
<222> (1)..(888)																
<400> 71																
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Met	Asn	Gly	Val	His	Asp	Leu	Gly	Gly	Met	Asp	Gly	Phe	Gly	Arg	Val	
1			5						10					15		
atg	gcg	gag	gcg	gac	gag	ccg	gtc	ttt	cat	gag	ccc	tgg	gaa	ggt	cgc	96
Met	Ala	Glu	Ala	Asp	Glu	Pro	Val	Phe	His	Glu	Pro	Trp	Glu	Gly	Arg	
20			25						30							
gtg	ttt	gcg	ctc	aac	atg	ctc	ggc	atc	ggg	cgc	gag	ccc	att	ccg	gtg	144
Val	Phe	Ala	Leu	Asn	Met	Leu	Gly	Ile	Gly	Arg	Glu	Pro	Ile	Pro	Val	
35			40						45							
gac	gcg	ctg	cgc	cat	cgc	att	gag	cg	atc	gag	ccg	tgg	cgc	tat	ctg	192
Asp	Ala	Leu	Arg	His	Arg	Ile	Glu	Arg	Ile	Glu	Pro	Trp	Arg	Tyr	Leu	
50			55						60							
acg	tcg	agc	tat	tac	gaa	cga	tgg	ctg	gcc	gaa	atg	gag	cag	gcc	atc	240
Thr	Ser	Ser	Tyr	Tyr	Glu	Arg	Trp	Leu	Ala	Glu	Met	Glu	Gln	Ala	Ile	
65			70					75			80					
atc	gat	gcg	ggc	acg	ctg	act	cct	gg	gaa	atc	gat	g	cga	atg	ggc	288
Ile	Asp	Ala	Gly	Thr	Leu	Thr	Pro	Gly	Glu	Ile	Asp	Ala	Arg	Met	Gly	
85			90						95							
gag	ctc	gaa	acg	gat	cct	gat	cg	cc	cca	ctg	cca	agg	act	gat	aac	336
Glu	Leu	Glu	Thr	Asp	Pro	Asp	Arg	Pro	Leu	Pro	Arg	Thr	Asp	Asn	Pro	
100			105						110							
gag	cat	gcc	gat	ggg	gt	g	cg	g	cg	tt	cg	cc	gc	gt	cc	384
Glu	His	Ala	Asp	Gly	Val	Ala	Ala	Ala	Leu	Arg	Ala	Gly	Ser	Pro	Val	
115			120						125							
acg	cgc	aag	att	cg	aag	cag	ccg	cgc	ttc	aca	atc	gg	gat	cg	gt	432
Thr	Arg	Lys	Ile	Arg	Lys	Gln	Pro	Arg	Phe	Thr	Ile	Gly	Asp	Arg	Val	
130			135						140							
gta	acg	cgc	aat	ctt	aat	ccg	cac	gg	cat	acg	cg	ct	cc	cg	cc	480
Val	Thr	Arg	Asn	Leu	Asn	Pro	His	Gly	His	Thr	Arg	Leu	Pro	Arg	Tyr	
145			150						155			160				
g	cg	cc	aag	cg	gg	gt	g	cg	tt	cg	ca	cc	gc	ca	cc	528
Ala	Arg	Gly	Lys	Arg	Gly	Val	Val	Thr	Leu	His	His	Gly	Ala	His	Val	
165			170						175							
ttt	ccg	gat	acg	aac	g	cg	ca	gg	ct	g	ca	cc	ca	ca	cc	576
Phe	Pro	Asp	Thr	Asn	Ala	His	Gly	Leu	Gly	Glu	His	Pro	Gln	His	Leu	
180			185						190							
tat	acg	gt	cg	ttt	cct	g	cg	cg	gag	cat	cc	ca	ca	cc	gg	624
Tyr	Thr	Val	Arg	Phe	Pro	Ala	Arg	Glu	Leu	Trp	Ser	Asp	Ala	Ala	Glu	
195			200						205							

ccg aaa gaa tcg ata atg atc gat ttg tgg gag agc tat ctt caa ccc Pro Lys Glu Ser Ile Met Ile Asp Leu Trp Glu Ser Tyr Leu Gln Pro	672
210 215 220	
gat atc ggc agc aaa gcg tcg tcg tcc gcg aaa ggc aaa gcg acg ccg Asp Ile Gly Ser Lys Ala Ser Ser Ala Lys Gly Lys Ala Thr Pro	720
225 230 235 240	
aaa gtt aag ccc gca atg gcc aag gca acc gcc aag gta agc gtc tcg Lys Val Lys Pro Ala Met Ala Lys Ala Thr Ala Lys Val Ser Val Ser	768
245 250 255	
gcc aag gcc aaa act cgg gga aag gcg gcg ccg aag gag cgt cca aaa Ala Lys Ala Lys Thr Arg Gly Lys Ala Ala Pro Lys Glu Arg Pro Lys	816
260 265 270	
ctg aaa cct gcg cga gcg acc tca gca gca tcc ggc ggc gaa aaa Leu Lys Pro Ala Arg Ala Ala Thr Ser Ala Ala Ser Gly Gly Glu Lys	864
275 280 285	
gct aag cga aag gcc aaa cga tga Ala Lys Arg Lys Ala Lys Arg 290 295	888

<210> 72  
 <211> 295  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Metagenome - beta unit nitrile hydratase - M49bd9

<400> 72

Met Asn Gly Val His Asp Leu Gly Gly Met Asp Gly Phe Gly Arg Val  
 1 5 10 15

Met Ala Glu Ala Asp Glu Pro Val Phe His Glu Pro Trp Glu Gly Arg  
 20 25 30

Val Phe Ala Leu Asn Met Leu Gly Ile Gly Arg Glu Pro Ile Pro Val  
 35 40 45

Asp Ala Leu Arg His Arg Ile Glu Arg Ile Glu Pro Trp Arg Tyr Leu  
 50 55 60

Thr Ser Ser Tyr Tyr Glu Arg Trp Leu Ala Glu Met Glu Gln Ala Ile  
 65 70 75 80

Ile Asp Ala Gly Thr Leu Thr Pro Gly Glu Ile Asp Ala Arg Met Gly  
 85 90 95

Glu Leu Glu Thr Asp Pro Asp Arg Pro Leu Pro Arg Thr Asp Asn Pro  
 100 105 110

Glu His Ala Asp Gly Val Ala Ala Leu Arg Ala Gly Ser Pro Val  
 115 120 125

Thr Arg Lys Ile Arg Lys Gln Pro Arg Phe Thr Ile Gly Asp Arg Val  
 130 135 140

Val Thr Arg Asn Leu Asn Pro His Gly His Thr Arg Leu Pro Arg Tyr  
145 150 155 160

Ala Arg Gly Lys Arg Gly Val Val Thr Leu His His Gly Ala His Val  
165 170 175

Phe Pro Asp Thr Asn Ala His Gly Leu Gly Glu His Pro Gln His Leu  
180 185 190

Tyr Thr Val Arg Phe Pro Ala Arg Glu Leu Trp Ser Asp Ala Ala Glu  
195 200 205

Pro Lys Glu Ser Ile Met Ile Asp Leu Trp Glu Ser Tyr Leu Gln Pro  
210 215 220

Asp Ile Gly Ser Lys Ala Ser Ser Ser Ala Lys Gly Lys Ala Thr Pro  
225 230 235 240

Lys Val Lys Pro Ala Met Ala Lys Ala Thr Ala Lys Val Ser Val Ser  
245 250 255

Ala Lys Ala Lys Thr Arg Gly Lys Ala Ala Pro Lys Glu Arg Pro Lys  
260 265 270

Leu Lys Pro Ala Arg Ala Ala Thr Ser Ala Ala Ser Gly Gly Glu Lys  
275 280 285

Ala Lys Arg Lys Ala Lys Arg  
290 295

<210> 73

<211> 630

<212> DNA

<213> Unknown

<220>

<223> Metagenome - beta unit nitrile hydratase - M6dE2

<220>

<221> CDS

<222> (1)..(630)

<400> 73

atg gac ggc att cat gat ctc ggt ggg atg agc ggg ttc ggt ctc gtg  
Met Asp Gly Ile His Asp Leu Gly Gly Met Ser Gly Phe Gly Leu Val  
1 5 10 15

48

gag atc gag ccc gat gag ccg gtg ttc cac gag ccc tgg gag gcg ctg  
Glu Ile Glu Pro Asp Glu Pro Val Phe His Glu Pro Trp Glu Ala Leu  
20 25 30

96

gtt ttc gct ctg atg act ctc ggt atc ggg aag ctc ggc gcg tac aac  
Val Phe Ala Leu Met Thr Leu Gly Ile Gly Lys Leu Gly Ala Tyr Asn  
35 40 45

144

gcc gat gag tac cgc cac tcg atc gag cgg atg gat ccg gcc cac tac  
Ala Asp Glu Tyr Arg His Ser Ile Glu Arg Met Asp Pro Ala His Tyr  
50 55 60

192

ctt gcg gcg acg tac tac gag cgc atg ctc acc ggc gtc gca acg ctc	240
Leu Ala Ala Thr Tyr Tyr Glu Arg Met Leu Thr Gly Val Ala Thr Leu	
65 70 75 80	
ctc gtc gag aag aac gtc gtt gcc cgc gac gag ctc gaa gcg cgc gcc	288
Leu Val Glu Lys Asn Val Val Ala Arg Asp Glu Leu Glu Ala Arg Ala	
85 90 95	
ggc ggg ccc ttc ccg ctg tca cgg ccg gtc gag cgg ccg acg gcg	336
Gly Gly Pro Phe Pro Leu Ser Arg Pro Val Ala Glu Arg Pro Thr Ala	
100 105 110	
gac ctt ccg ccc cag cca caa cca cgc ttc gcg gtc ggg gat cgg gtc	384
Asp Leu Arg Pro Gln Pro Gln Pro Arg Phe Ala Val Gly Asp Arg Val	
115 120 125	
gtc gtg cgc gac atc cac ccg gcc ggg cat act cgt gtg ccg cgc tac	432
Val Val Arg Asp Ile His Pro Ala Gly His Thr Arg Val Pro Arg Tyr	
130 135 140	
gtg cgg ggc aag cgc ggg acc gtc gtg cac gtc gcg ccg aaa ttc tcg	480
Val Arg Gly Lys Arg Gly Thr Val Val His Val Ala Pro Lys Phe Ser	
145 150 155 160	
ttc ccc gac acg gcc gcg cac ggg ctg acc cat cgg agc gag cac acg	528
Phe Pro Asp Thr Ala Ala His Gly Leu Thr His Arg Ser Glu His Thr	
165 170 175	
tat cac gtg gaa ttc gtc gcg agt gac ctt tgg gcc gac gtg gcc ggg	576
Tyr His Val Glu Phe Val Ala Ser Asp Leu Trp Ala Asp Val Ala Gly	
180 185 190	
agc aat gag agc gta ctc gtg gac ctg tgg gac ggc tat ctg gag ggc	624
Ser Asn Glu Ser Val Leu Val Asp Leu Trp Asp Gly Tyr Leu Glu Gly	
195 200 205	
gca tga	630
Ala	

<210> 74  
 <211> 209  
 <212> PRT  
 <213> Unknown

<220>

<223> Metagenome - beta unit nitrile hydratase - M6dE2

<400> 74

Met Asp Gly Ile His Asp Leu Gly Gly Met Ser Gly Phe Gly Leu Val  
 1 5 10 15

Glu Ile Glu Pro Asp Glu Pro Val Phe His Glu Pro Trp Glu Ala Leu  
 20 25 30

val Phe Ala Leu Met Thr Leu Gly Ile Gly Lys Leu Gly Ala Tyr Asn  
 35 40 45

Ala Asp Glu Tyr Arg His Ser Ile Glu Arg Met Asp Pro Ala His Tyr  
 50 55 60

Leu Ala Ala Thr Tyr Tyr Glu Arg Met Leu Thr Gly Val Ala Thr Leu  
 65 70 75 80

Leu Val Glu Lys Asn Val Val Ala Arg Asp Glu Leu Glu Ala Arg Ala  
85 90 95

Gly Gly Pro Phe Pro Leu Ser Arg Pro Val Ala Glu Arg Pro Thr Ala  
100 105 110

Asp Leu Arg Pro Gln Pro Gln Pro Arg Phe Ala Val Gly Asp Arg Val  
115 120 125

Val Val Arg Asp Ile His Pro Ala Gly His Thr Arg Val Pro Arg Tyr  
130 135 140

Val Arg Gly Lys Arg Gly Thr Val Val His Val Ala Pro Lys Phe Ser  
145 150 155 160

Phe Pro Asp Thr Ala Ala His Gly Leu Thr His Arg Ser Glu His Thr  
165 170 175

Tyr His Val Glu Phe Val Ala Ser Asp Leu Trp Ala Asp Val Ala Gly  
180 185 190

Ser Asn Glu Ser Val Leu Val Asp Leu Trp Asp Gly Tyr Leu Glu Gly  
195 200 205

Ala

<210> 75

<211> 651

<212> DNA

<213> Unknown

<220>

<223> Metagenome - beta unit nitrile hydratase - M25A18

<220>

<221> CDS

<222> (1)...(651)

<400> 75

atg cgc ggc acg cac gat ctc ggc gga ttg ccc gcc ggc ccg gtg gac 48  
Met Arg Gly Thr His Asp Leu Gly Gly Leu Pro Ala Gly Pro Val Asp  
1 5 10 15

acc gct ccc cac gaa ccg acc ttc tgg gaa aag cag gtg gac gcg atc 96  
Thr Ala Pro His Glu Pro Thr Phe Trp Glu Lys Gln Val Asp Ala Ile  
20 25 30

cac ggc ctg ctc ggc gat tcc aag cgc cgc atc acg ctg cgc gac gag 144  
His Gly Leu Leu Gly Asp Ser Lys Arg Arg Ile Thr Leu Arg Asp Glu  
35 40 45

aac cgc ctc tat atc gaa tcg ctc ggc gac gac gtc tac aac acg ctc 192  
Asn Arg Leu Tyr Ile Glu Ser Leu Gly Asp Asp Val Tyr Asn Thr Leu  
50 55 60

ggc tat tac gag cgc tgg acc gcc gcc atg tgc cgc cag ctc atc gac 240  
Gly Tyr Tyr Glu Arg Trp Thr Ala Ala Met Cys Arg Gln Leu Ile Asp  
65 70 75 80

aag ggc gtc acg cag gac gag atc gac gcc aag atc gcc gag ctg Lys Gly Val Leu Thr Gln Asp Glu Ile Asp Ala Lys Ile Ala Glu Leu 85 90 95	288
cgc gcc cgc ggc gtc ggc gcg gga cga cga cga aac ggc ctg caa acc Arg Ala Arg Gly Val Gly Ala Gly Arg Arg Arg Asn Gly Leu Gln Thr 100 105 110	336
gtg agc gcc gat ctg gcc gat ctg gcc atc gcg ccg cgc ttc gcc Val Ser Ala Asp Leu Ala Asp Leu Ala Ile Ala Pro Arg Phe Ala 115 120 125	384
gcc ggc gac cgc gtg cgg gtg cgc gac gat tat ccg ccc ggg cac atc Ala Gly Asp Arg Val Arg Asp Asp Tyr Pro Pro Gly His Ile 130 135 140	432
cgc acg ccg gtc tat gtg cgc ggc aag acg ggc gtg gtg acg cgc tgc Arg Thr Pro Val Tyr Val Arg Gly Lys Thr Gly Val Val Thr Arg Cys 145 150 155 160	480
ttc ggc gcg ttc aag aac ccg gaa ttg ctc gcc atc ggc aag gac ggc Phe Gly Ala Phe Lys Asn Pro Glu Leu Leu Ala Ile Gly Lys Asp Gly 165 170 175	528
ctg ccc aag aaa att ctc tac gaa gtg cgc ttc aag cag acc gat ctc Leu Pro Lys Lys Ile Leu Tyr Glu Val Arg Phe Lys Gln Thr Asp Leu 180 185 190	576
tgg ccc gac tat gcc ggg ccg gcg acc gat acg ctg ctg atc gac atc Trp Pro Asp Tyr Ala Gly Pro Ala Thr Asp Thr Leu Leu Ile Asp Ile 195 200 205	624
tac gaa cat tgg ctg agc gac gcg tga Tyr Glu His Trp Leu Ser Asp Ala 210 215	651

<210> 76  
 <211> 216  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Metagenome - beta unit nitrile hydratase - M25A18

<400> 76

Met Arg Gly Thr His Asp Leu Gly Gly Leu Pro Ala Gly Pro Val Asp  
1 5 10 15

Thr Ala Pro His Glu Pro Thr Phe Trp Glu Lys Gln Val Asp Ala Ile  
20 25 30

His Gly Leu Leu Gly Asp Ser Lys Arg Arg Ile Thr Leu Arg Asp Glu  
35 40 45

Asn Arg Leu Tyr Ile Glu Ser Leu Gly Asp Asp Val Tyr Asn Thr Leu  
50 55 60

Gly Tyr Tyr Glu Arg Trp Thr Ala Ala Met Cys Arg Gln Leu Ile Asp  
65 70 75 80

Lys Gly Val Leu Thr Gln Asp Glu Ile Asp Ala Lys Ile Ala Glu Leu  
85 90 95

Arg Ala Arg Gly Val Gly Ala Gly Arg Arg Arg Asn Gly Leu Gln Thr  
100 105 110

Val Ser Ala Asp Leu Ala Ala Asp Leu Ala Ile Ala Pro Arg Phe Ala  
115 120 125

Ala Gly Asp Arg Val Arg Val Arg Asp Asp Tyr Pro Pro Gly His Ile  
130 135 140

Arg Thr Pro Val Tyr Val Arg Gly Lys Thr Gly Val Val Thr Arg Cys  
145 150 155 160

Phe Gly Ala Phe Lys Asn Pro Glu Leu Leu Ala Ile Gly Lys Asp Gly  
165 170 175

Leu Pro Lys Lys Ile Leu Tyr Glu Val Arg Phe Lys Gln Thr Asp Leu  
180 185 190

Trp Pro Asp Tyr Ala Gly Pro Ala Thr Asp Thr Leu Leu Ile Asp Ile  
195 200 205

Tyr Glu His Trp Leu Ser Asp Ala  
210 215

<210> 77

<211> 657

<212> DNA

<213> Unknown

<220>

<223> Metagenome - beta unit nitrile hydratase - M50bd9

<220>

<221> CDS

<222> (1)..(657)

<400> 77

atg aac ggc atg cat gac atg ggc ggc atg cac ggc atg gga ccc att 48  
Met Asn Gly Met His Asp Met Gly Gly Met His Gly Met Gly Pro Ile  
1 5 10 15

cag atc gag aag gac gag tcg ccc ttc cat gcg cgc tgg gaa ggc cgg 96  
Gin Ile Glu Lys Asp Glu Ser Pro Phe His Ala Arg Trp Glu Gly Arg  
20 25 30

gcg caa gcg atg tac aac gcc att gcg gcc acg ggc aga ctg gtg ctt 144  
Ala Gln Ala Met Tyr Asn Ala Ile Ala Ala Thr Gly Arg Leu Val Leu  
35 40 45

ggc ggt aga ccc aca cgg gaa ggg ttc ccg ccg gcc gaa tat ctc cgc 192  
Gly Arg Pro Thr Arg Glu Gly Phe Pro Pro Ala Glu Tyr Leu Arg  
50 55 60

atg agc tac tat gaa ttg ggt ttc agg gtc ctg gtc gag gac ttg gtc 240  
Met Ser Tyr Tyr Glu Leu Gly Phe Arg Val Leu Val Glu Asp Leu Val  
65 70 75 80

ctg aac ggt ttg gtg acg cgc gcg gaa atc acg agc ggc cgt ccg gca 288  
Leu Asn Gly Leu Val Thr Arg Ala Glu Ile Thr Ser Gly Arg Pro Ala  
85 90 95

aag ggg gct gca aag tcg acg ccc gca atc acc gcc gcc acc gcg cag Lys Gly Ala Ala Lys Ser Thr Pro Ala Ile Thr Ala Ala Thr Ala Gln 100 105 110	336
gca tat atg ttc gcg ctc aaa tcg acc cgg cga gac gta ccg gtc acg Ala Tyr Met Phe Ala Leu Lys Ser Thr Arg Arg Asp Val Pro Val Thr 115 120 125	384
gct cgt ttc caa gtc ggt cag cgt gtg cgc gct cgc aac atc aat ccg Ala Arg Phe Gln Val Gly Gln Arg Val Arg Ala Arg Asn Ile Asn Pro 130 135 140	432
gtc acc cat acg cgc ctg ccc cgt tac gct cgc ggc aaa ttc ggc gtt Val Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly Lys Phe Gly Val 145 150 155 160	480
atc gaa cgt gac cac ggt gtt tac agg ttc gac gat tcc ttt gcc acg Ile Glu Arg Asp His Gly Val Tyr Arg Phe Asp Asp Ser Phe Ala Thr 165 170 175	528
tcc ggc gac gag aag ccc cag cac gtt tat tct gtg cgc ttc gcg gcg Ser Gly Asp Glu Lys Pro Gln His Val Tyr Ser Val Arg Phe Ala Ala 180 185 190	576
cgc gaa cta tgg ggc gaa gcc gcg ccg cca gat gct gtc tat atc Arg Glu Leu Trp Gly Glu Ala Ala Pro Pro Arg Asp Ala Val Tyr Ile 195 200 205	624
gaa atc tgg gat gac aac ctt gag cca gcg tga Glu Ile Trp Asp Asp Asn Leu Glu Pro Ala 210 215	657

<210> 78  
 <211> 218  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Metagenome - beta unit nitrile hydratase - M50bd9

<400> 78

Met Asn Gly Met His Asp Met Gly Gly Met His Gly Met Gly Pro Ile  
1 5 10 15

Gln Ile Glu Lys Asp Glu Ser Pro Phe His Ala Arg Trp Glu Gly Arg  
20 25 30

Ala Gln Ala Met Tyr Asn Ala Ile Ala Ala Thr Gly Arg Leu Val Leu  
35 40 45

Gly Gly Arg Pro Thr Arg Glu Gly Phe Pro Pro Ala Glu Tyr Leu Arg  
50 55 60

Met Ser Tyr Tyr Glu Leu Gly Phe Arg Val Leu Val Glu Asp Leu Val  
65 70 75 80

Leu Asn Gly Leu Val Thr Arg Ala Glu Ile Thr Ser Gly Arg Pro Ala  
85 90 95

Lys Gly Ala Ala Lys Ser Thr Pro Ala Ile Thr Ala Ala Thr Ala Gln  
100 105 110

Ala Tyr Met Phe Ala Leu Lys Ser Thr Arg Arg Asp Val Pro Val Thr  
115 120 125

Ala Arg Phe Gln Val Gly Gln Arg Val Arg Ala Arg Asn Ile Asn Pro  
130 135 140

Val Thr His Thr Arg Leu Pro Arg Tyr Ala Arg Gly Lys Phe Gly Val  
145 150 155 160

Ile Glu Arg Asp His Gly Val Tyr Arg Phe Asp Asp Ser Phe Ala Thr  
165 170 175

Ser Gly Asp Glu Lys Pro Gln His Val Tyr Ser Val Arg Phe Ala Ala  
180 185 190

Arg Glu Leu Trp Gly Glu Ala Ala Pro Pro Arg Asp Ala Val Tyr Ile  
195 200 205

Glu Ile Trp Asp Asp Asn Leu Glu Pro Ala  
210 215

<210> 79

<211> 696

<212> DNA

<213> Unknown

<220>

<223> Metagenome - beta unit nitrile hydratase - M3aG10

<220>

<221> CDS

<222> (1)..(696)

<400> 79

atg gat cca acg agg cgt agt ttc ctg gcg tct acc gtt gcc ctg acc 48  
Met Asp Pro Thr Arg Arg Ser Phe Leu Ala Ser Thr Val Ala Leu Thr  
1 5 10 15

ggc ggc gca gct atc ccc gat ctg gct cat gcg gca gac cac gac cac 96  
Gly Gly Ala Ala Ile Pro Asp Leu Ala His Ala Ala Asp His Asp His  
20 25 30

cag cat caa gat ttg ccg tcc gat ctg gcg ctg cgg gtg aag tcg ctc 144  
Gln His Gln Asp Leu Pro Ser Asp Leu Ala Leu Arg Val Lys Ser Leu  
35 40 45

gaa tcg ctg ctt gtc gag aag ggg ctg gtg gag cga gca gcg ctc gac 192  
Glu Ser Leu Leu Val Glu Lys Gly Leu Val Glu Arg Ala Ala Leu Asp  
50 55 60

gcg ctg gtg gac acc tac gag cac aaa gtc ggg ccg cga aac gga gcg 240  
Ala Leu Val Asp Thr Tyr Glu His Lys Val Gly Pro Arg Asn Gly Ala  
65 70 75 80

cgc gtt gtc gcg cgg gcc tgg gtt gac ccg gac tac aag caa cgg tta 288  
Arg Val Val Ala Arg Ala Trp Val Asp Pro Asp Tyr Lys Gln Arg Leu  
85 90 95

ttc gcg aac ggt acc gcc gca gtc gcg gag ttc ggc tac tcc ggc tcg 336  
Phe Ala Asn Gly Thr Ala Ala Val Ala Glu Phe Gly Tyr Ser Gly Ser  
100 105 110

cag ggc gct gac atc cgg gtc gtc gaa aac acg gcc act gta cat aac Gln Gly Ala Asp Ile Arg Val Val Glu Asn Thr Ala Thr Val His Asn 115 120 125	384
ctc gtc gtg tgc acg ctg tgc tct tgt tat ccc tgg ccg gtg ctg ggc Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly 130 135 140	432
ttg ccg ccg gtc tgg tac aag tcc gcg ccc tat cgg tct cgc gtg gtg Leu Pro Pro Val Trp Tyr Lys Ser Ala Pro Tyr Arg Ser Arg Val Val 145 150 155 160	480
atc gat ccg cga ggt gtg ctg cgc gag ttc ggc gtg gtg ctg ccg gac Ile Asp Pro Arg Gly Val Leu Arg Glu Phe Gly Val Val Leu Pro Asp 165 170 175	528
cat atc gaa gtg cgt gtc tat gac agc acg gcg gag caa cgc tat cta His Ile Glu Val Arg Val Tyr Asp Ser Thr Ala Glu Gln Arg Tyr Leu 180 185 190	576
gtg ctg ccg gag cgg ccg gcc gga acc gaa aac ctg aca gaa gaa gcg Val Leu Pro Glu Arg Pro Ala Gly Thr Glu Asn Leu Thr Glu Glu Ala 195 200 205	624
ctg gcg ctg ctg gtg acg cgc gac gcg atg att ggc gtg gcc aag gtc Leu Ala Leu Leu Val Thr Arg Asp Ala Met Ile Gly Val Ala Lys Val 210 215 220	672
gcg ccg ccg gga ggc cgc gga tga Ala Pro Pro Gly Gly Arg Gly 225 230	696
<210> 80 <211> 231 <212> PRT <213> Unknown	
<220> <223> Metagenome - beta unit nitrile hydratase - M3aG10	
<400> 80	
Met Asp Pro Thr Arg Arg Ser Phe Leu Ala Ser Thr Val Ala Leu Thr 1 5 10 15	
Gly Gly Ala Ala Ile Pro Asp Leu Ala His Ala Ala Asp His Asp His 20 25 30	
Gln His Gln Asp Leu Pro Ser Asp Leu Ala Leu Arg Val Lys Ser Leu 35 40 45	
Glu Ser Leu Leu Val Glu Lys Gly Leu Val Glu Arg Ala Ala Leu Asp 50 55 60	
Ala Leu Val Asp Thr Tyr Glu His Lys Val Gly Pro Arg Asn Gly Ala 65 70 75 80	
Arg Val Val Ala Arg Ala Trp Val Asp Pro Asp Tyr Lys Gln Arg Leu 85 90 95	
Phe Ala Asn Gly Thr Ala Ala Val Ala Glu Phe Gly Tyr Ser Gly Ser 100 105 110	

Gln Gly Ala Asp Ile Arg Val Val Glu Asn Thr Ala Thr Val His Asn  
115 120 125

Leu Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly  
130 135 140

Leu Pro Pro Val Trp Tyr Lys Ser Ala Pro Tyr Arg Ser Arg Val Val  
145 150 155 160

Ile Asp Pro Arg Gly Val Leu Arg Glu Phe Gly Val Val Leu Pro Asp  
165 170 175

His Ile Glu Val Arg Val Tyr Asp Ser Thr Ala Glu Gln Arg Tyr Leu  
180 185 190

Val Leu Pro Glu Arg Pro Ala Gly Thr Glu Asn Leu Thr Glu Glu Ala  
195 200 205

Leu Ala Leu Leu Val Thr Arg Asp Ala Met Ile Gly Val Ala Lys Val  
210 215 220

Ala Pro Pro Gly Gly Arg Gly  
225 230

<210> 81

<211> 327

<212> DNA

<213> Unknown

<220>

<223> Metagenome - p12K unit

<220>

<221> CDS

<222> (1)..(327)

<400> 81

atg aaa gat agc ccg gtc ttt cgc gag ccg tgg gaa gcg cag gcg ttt  
Met Lys Asp Ser Pro Val Phe Arg Glu Pro Trp Glu Ala Gln Ala Phe  
1 5 10 15

gcg ttg gcg atc tcg ttg caa gac cgt ggc gtc ttc acg cga gac gaa  
Ala Leu Ala Ile Ser Leu Gln Asp Arg Gly Val Phe Thr Arg Asp Glu  
20 25 30

tgg gcg gcg gca ctc ggc gat gaa atc aag aag gcg caa gct gcc ggc  
Trp Ala Ala Ala Leu Gly Asp Glu Ile Lys Lys Ala Gln Ala Ala Gly  
35 40 45

gat ccc gat acg ggc gag act tat tac cat cat tgg atg gca gcg ctc  
Asp Pro Asp Thr Gly Glu Thr Tyr Tyr His His Trp Met Ala Ala Leu  
50 55 60

gaa cgg ctg att gca gcc aag ggt gtt gcc gat acg cag acg ctc gcg  
Glu Arg Leu Ile Ala Ala Lys Gly Val Ala Asp Thr Gln Thr Leu Ala  
65 70 75 80

cgc aca cgc gac gcc tgg cag cac gcc tgt gcg cga acg ccg cat ggc  
Arg Thr Arg Asp Ala Trp Gln His Ala Cys Ala Arg Thr Pro His Gly  
85 90 95

gct cca atc gag cta aga ccg gac gac ttc agg aat tga 327  
Ala Pro Ile Glu Leu Arg Pro Asp Asp Phe Arg Asn  
100 105

<210> 82  
<211> 108  
<212> PRT  
<213> Unknown

<220>  
<223> Metagenome - p12K unit

<400> 82

Met Lys Asp Ser Pro Val Phe Arg Glu Pro Trp Glu Ala Gln Ala Phe  
1 5 10 15

Ala Leu Ala Ile Ser Leu Gln Asp Arg Gly Val Phe Thr Arg Asp Glu  
20 25 30

Trp Ala Ala Ala Leu Gly Asp Glu Ile Lys Lys Ala Gln Ala Ala Gly  
35 40 45

Asp Pro Asp Thr Gly Glu Thr Tyr Tyr His His Trp Met Ala Ala Leu  
50 55 60

Glu Arg Leu Ile Ala Ala Lys Gly Val Ala Asp Thr Gln Thr Leu Ala  
65 70 75 80

Arg Thr Arg Asp Ala Trp Gln His Ala Cys Ala Arg Thr Pro His Gly  
85 90 95

Ala Pro Ile Glu Leu Arg Pro Asp Asp Phe Arg Asn  
100 105

<210> 83  
<211> 321  
<212> DNA  
<213> Unknown

<220>  
<223> Metagenome - p12K unit

<220>  
<221> CDS  
<222> (1)..(321)

<400> 83

atg aga aca gtt gct gag caa atc gct gat ctt gct agt ccg gct 48  
Met Arg Thr Val Ala Glu Gln Ile Ala Ala Asp Leu Ala Ser Pro Ala  
1 5 10 15

gct att ccg cgc cgc aac ggc gag ccg gtc ttc gac gag cct tgg gaa 96  
Ala Ile Pro Arg Arg Asn Gly Glu Pro Val Phe Asp Glu Pro Trp Glu  
20 25 30

agt cgt gct ttt ggg ata gct gtc gcc ctt tcc gag ggt ggc ctc tat 144  
Ser Arg Ala Phe Gly Ile Ala Val Ala Leu Ser Glu Gly Gly Leu Tyr  
35 40 45

tca tgg gat gaa ttt cgc gat tgc ctg att gct gaa atc aca gca gcg  
Ser Trp Asp Glu Phe Arg Asp Cys Leu Ile Ala Glu Ile Thr Ala Ala  
50 55 60 192

gat gcg cgc ggc gag cat acg agc tat tac gaa cgg ttt ctc gcc gcc  
Asp Ala Arg Gly Glu His Thr Ser Tyr Tyr Glu Arg Phe Leu Ala Ala  
65 70 75 80 240

ctg cag cat ctg ctc gcg gcc aaa cgc ctc tgc act ccc gat gaa gtc  
Leu Gln His Leu Leu Ala Ala Lys Arg Leu Cys Thr Pro Asp Glu Val  
85 90 95 288

gag cgg cgg atg aac act agc gca ggc acc tga  
Glu Arg Arg Met Asn Thr Ser Ala Gly Thr  
100 105 321

<210> 84

<211> 106

<212> PRT

<213> Unknown

<220>  
<223> Metagenome - p12K unit

<400> 84

Met Arg Thr Val Ala Glu Gln Ile Ala Ala Asp Leu Ala Ser Pro Ala  
1 5 10 15

Ala Ile Pro Arg Arg Asn Gly Glu Pro Val Phe Asp Glu Pro Trp Glu  
20 25 30

Ser Arg Ala Phe Gly Ile Ala Val Ala Leu Ser Glu Gly Gly Leu Tyr  
35 40 45

Ser Trp Asp Glu Phe Arg Asp Cys Leu Ile Ala Glu Ile Thr Ala Ala  
50 55 60

Asp Ala Arg Gly Glu His Thr Ser Tyr Tyr Glu Arg Phe Leu Ala Ala  
65 70 75 80

Leu Gln His Leu Leu Ala Ala Lys Arg Leu Cys Thr Pro Asp Glu Val  
85 90 95

Glu Arg Arg Met Asn Thr Ser Ala Gly Thr  
100 105

<210> 85  
 <211> 426  
 <212> DNA  
 <213> Unknown  
  
 <220>  
 <223> Metagenome - p12K unit  
  
 <220>  
 <221> CDS  
 <222> (1)..(426)  
  
 <400> 85

atg aca acc ttg agc cag cgt gaa gcg gcc ccc tcg gcc gag ctt ctt	48
Met Thr Thr Leu Ser Gln Arg Glu Ala Ala Pro Ser Ala Glu Leu Leu	
1 5 10 15	
gac cta ccg caa ctt cca agc gac acc gac ggc ccc gtc ttc gcg gaa	96
Asp Leu Pro Gln Leu Pro Ser Asp Thr Asp Gly Pro Val Phe Ala Glu	
20 25 30	
cct tgg gaa gcg gaa gcg ttt gcg ctt gcc gta agt ctt tca gag caa	144
Pro Trp Glu Ala Glu Ala Phe Ala Leu Ala Val Ser Leu Ser Glu Gln	
35 40 45	
gga cat ttc acg tgg aag gaa tgg gca gca acg ctc gcc gat gaa ctg	192
Gly His Phe Thr Trp Lys Glu Trp Ala Ala Thr Leu Ala Asp Glu Leu	
50 55 60	
gag ggc gcc gcc aat cgc ggc gag ccg gat gac ggt acg cat tat tat	240
Glu Gly Ala Ala Asn Arg Gly Glu Pro Asp Asp Gly Thr His Tyr Tyr	
65 70 75 80	
gag tac tgg ctg acg gcc ctg gaa agg ctg gtt acg atc aag ggc ctg	288
Glu Tyr Trp Leu Thr Ala Leu Glu Arg Leu Val Thr Ile Lys Gly Leu	
85 90 95	
aca gat cag caa gcg atg cgc gag cgc aaa gag gcg tgg gaa gaa gcc	336
Thr Asp Gln Gln Ala Met Arg Glu Arg Lys Glu Ala Trp Glu Glu Ala	
100 105 110	
tat cgc cat acc ccg cat ggc gcg cca gtt gaa ctt atg tct ccg ctc	384
Tyr Arg His Thr Pro His Gly Ala Pro Val Glu Leu Met Ser Pro Leu	
115 120 125	
gat caa agc cgg ata gcc gaa gag gac agc gaa tcc tca tag	426
Asp Gln Ser Arg Ile Ala Glu Glu Asp Ser Glu Ser Ser	
130 135 140	

<210> 86  
 <211> 141  
 <212> PRT  
 <213> Unknown  
  
 <220>  
 <223> Metagenome - p12K unit  
  
 <400> 86

Met Thr Thr Leu Ser Gln Arg Glu Ala Ala Pro Ser Ala Glu Leu Leu	
1 5 10 15	
Asp Leu Pro Gln Leu Pro Ser Asp Thr Asp Gly Pro Val Phe Ala Glu	
20 25 30	
Pro Trp Glu Ala Glu Ala Phe Ala Leu Ala Val Ser Leu Ser Glu Gln	
35 40 45	

Gly His Phe Thr Trp Lys Glu Trp Ala Ala Thr Leu Ala Asp Glu Leu  
50 55 60

Glu Gly Ala Ala Asn Arg Gly Glu Pro Asp Asp Gly Thr His Tyr Tyr  
65 70 75 80

Glu Tyr Trp Leu Thr Ala Leu Glu Arg Leu Val Thr Ile Lys Gly Leu  
85 90 95

Thr Asp Gln Gln Ala Met Arg Glu Arg Lys Glu Ala Trp Glu Glu Ala  
100 105 110

Tyr Arg His Thr Pro His Gly Ala Pro Val Glu Leu Met Ser Pro Leu  
115 120 125

Asp Gln Ser Arg Ile Ala Glu Glu Asp Ser Glu Ser Ser  
130 135 140